

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

Type of Search

Vendors and cost where applicable

Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: _____	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: _____	Bibliographic _____	Dr. Link _____
Date Completed: _____	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems _____
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) _____

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 29, 2001, 19:01:33 ; Search time 1433.84 Seconds
(without alignments)
1739.357 Million cell updates/sec

Title: US-09-249-011-5

Perfect score: 405
Sequence: 1 atgggttggaactgtatcat.....ccctgtcacgcgtctctca 405

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 3078962356 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba1: *
2: gb_ba2: *
3: gb_ba3: *
4: gb_ba4: *
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92: em_pi: *
93: em_pi: *
94: em_pi: *
95: em_pi: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	289.6	71.5	805	56	AF238196 Synthetic
2	272.2	67.2	446	10	108288 Sequence 4
3	272.2	67.2	462	95	S78361 AHT107 VH r
4	251.4	62.1	405	92	HSIGHX11 X65893 H.sapiens m
5	248.2	61.3	433	9	AR024343 Sequence AR024343
6	248.2	61.3	433	9	AR045196 Sequence AR045196
7	245	60.5	405	10	I31950 Sequence 68
8	245	60.5	405	10	I78362 Sequence 68
9	245	60.5	405	10	I78617 Sequence 68
10	245	60.5	405	92	HSBUD114H Z46348 Homo sapien
11	245	60.5	405	94	MUSIGHM195 Mus muscul


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/cell_type="pre-B"
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misc_feature
58. 352
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353. 366
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367. 405
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BASE COUNT      95 a      106 c      120 g      84 t
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Matches 309; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 1 atgggttgaaactgtatcatcttcttcttggttaccaagctacaggtgtgcaactccag 60
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Db 1 ATGGACTGGACCTGGAGGCTCTCTTTGGTGCGAGCAGCAGCAAGTGGCCACTCCAG 60

QY 61 gtccagctgtgtcagctctgtggctgtgaagaaagcctggagctcagtgaaagtgtcc 120
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QY 121 tgcgaagcttcggctacacattcactgattatgctatagagtggtgagacagctctc 180
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Db 121 TGCAGAGCTTGTGATACCTTCACCTAGCTATGCTATGCTATGGGTGGCCAGGCCCC 180

QY 181 ggacaggcctcagatgtgagtgatlaataattactaataataacataacacac 240
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Db 181 GGACAAAGCCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240

QY 241 cagaagtttaagggaagccacaatgactgtagaacaagtcgaagcagacagcctatag 300
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Db 241 CAGAAGTTTCAAGGCGAGAGTACCATTTACCAAGGACACATCCGCGAGCACAGCCTACATG 300

QY 301 gaacttagtcttcttgagatcagatagacggcggttattactgtgcaagagcgccctg 360
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Db 301 GAGCTGAGCAGCTGAGATCTGAGAGACAGCGCTGTATTTACTGTGCGAGGATTAACCC 360

QY 361 tataagactactgtgtgtcgaagtaacctgtgcaacgctctccca 405
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Db 361 TATATGCACTACTGGGGCAGGAACCTGTGTCAACGCTCTCTCA 405

RESULT 5
AR024343 433 bp DNA PAT 05-DEC-1998
LOCUS Sequence 111 from patent US 5795965.
DEFINITION AR024343
ACCESSION AR024343
VERSION AR024343.1 GI:3977637
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 433)
AUTHORS Tsuchiya,M., Sato,K., Bendig,M.Margaret, Jones,S.Tarran and
        Saidanba,J.William.
        Reshaped human to human interleukin-6 receptor
        Patent: US 5795965-A 111 18-AUG-1998;
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BASE COUNT      94 a      108 c      128 g      103 t
ORIGIN

Query Match
Best Local Similarity 61.3% Score 248.2; DB 9; Length 433;
Matches 307; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

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Matches 307; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

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QY 61 gtccagctgtgtcagctctgtggctgtgaagaaagcctggagctcagtgaaagtgtcc 120
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QY 121 tgcgaagcttcggctacacattcactgattatgctatagagtggtgagacagctctc 180
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QY 301 gaacttagtcttcttgagatcagatagacggcggttattactgtgcaagagcgccctg 360
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Db 316 GAGCTGAGCAGCTGAGATCTGAGAGACAGCGCTGTATTTACTGTGCGAGGAGGATTAAC 375

QY 361 tataagactactgtgtgtcgaagtaacctgtgcaacgctctccca 405
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Db 376 CGCTTGTCTACTGGGGCAGGAACCTGTGTCAACGCTCTCTCA 420

RESULT 6
AR045196 433 bp DNA PAT 29-SEP-1999
LOCUS Sequence 111 from patent US 5817790.
DEFINITION AR045196
ACCESSION AR045196
VERSION AR045196.1 GI:5966661
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 433)
AUTHORS Tsuchiya,M., Sato,K., Bendig,M.Margaret, Jones,S.Tarran and
        Saidanba,J.William.
        Reshaped human antibody to human interleukin-6 receptor
        Patent: US 5817790-A 111 06-OCT-1998;
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BASE COUNT      94 a      108 c      128 g      103 t
ORIGIN

Query Match
Best Local Similarity 75.8% Score 248.2; DB 9; Length 433;
Matches 307; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

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Oy	* 241	cagaagtttaagggaagcccaatgactgtgagacaagtgcacaaaccttatgt	300
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Oy	301	gaacttagtctcttgagatcctgagatacggccgittattactgtgcaagacggcgcttg	360
Dd	316	GAGCTGACACAGTCTGTAGATCTCGAACAACACGGCTGTGTATTACTGTGCAGGGGGGTAAAC	375
Oy	361	tatatgactactgggtgcgaagtaccctctgtcacgcgtctctca	405
Dd	376	CGCTTGCTTACTGGGGCCAGGGAAACCTGTGTACACGTCCTCTCA	420
RESULT	7		
LOCUS	IJ1950	405 bp	DNA
DEFINITION	Sequence 68 from patent US 5585089.	PAT	06-FEB-1997
ACCESSION	IJ1950		
VERSION	IJ1950.1	GI:1822741	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 405)		
TITLE	Queen,C.L. and Sellick,H.E.		
JOURNAL	Humanized immunoglobulins		
FEATURES	Patent: US 5585089-A 68 17-DEC-1996;		
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DB	1	ATGGAGTAGAGCTGGATCTTCTCTCTCCCTGTGACGAAGCTGCAGCGCTCCACTTGTAG	60
QY	61	gtccagctcgtgtgcaagctctgaggtcgaagtgaaagacccctggagctcagtgaaagtgtcc	120
DB	61	GTCCAGCTTTCACACAGTCCAGGACCTGAGGCTGGGAAACCTGGGGCCCTCAGTGAAGATATCC	120
QY	121	tgcgaagcttcgcggtacacatcattcaatgtattgtctatacagtgagggttgaaagagctcct	180
DB	121	TGCAAGGCTTTCGTGATTACACATTCCTGCTCAACATGCACTGGGTGTAAGACAGCCAT	180
QY	181	ggacagggccctcagatggaatggagttatataattactatgataaatacaactacaac	240
DB	181	GGAAGAGGCTTGTAGTGCATTTGGATATATTATTTATCTTTACATAGTGCTGTACTGGCTTACAC	240
QY	241	cagaaagtttaaaggaggaagccacaatlgactgtgagaagaagtcgacgagacagaactatag	300
DB	241	CAGAAGTTCAGAGCAAGCAAGGCCACATTTGACTGTAGACAAATTCCTCCAGCAGACAGCTAAG	300
QY	301	gaactagtcttccttgagatcctgagagataaagccggttatactatgycgaaagacgagctcgt	360
DB	301	GACGTCGCCAGGCTACACATCTGAGGACCTGTGCAAGTCTATTACTGTGCAAGAGGGGCCCC	360
QY	361	tatatgactactagggtgcaagtagtaacctgtgcaaccttctctca	405
DB	361	GCTATGGACTACTGGGGGTCAAGCAACTGATCACCCTCTCCTCA	405
RESULT	8		
LOCUS	I78562	405 bp	DNA
DEFINITION	Sequence 68 from patent US 5693761.		PAT
ACCESSION	I78562		
VERSION	I78562.1	GI:3014716	

KEYWORDS	unknown.
SOURCE	unknown.
ORGANISM	unknown.
REFERENCE	unclassified.
AUTHORS	1 (bases 1 to 405)
TITLE	Queen,C.I., Schneider,W.P. and Selick,H.E.
JOURNAL	Polynucleotides encoding improved humanized immunoglobulins
FEATURES	Patent: US 5693761 A 68 02-Dec-1997;
source	location/Qualifiers
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BASE COUNT	101 a 106 c 105 g 93 t
ORIGIN	

Query Match	60.5%	Score 245	DB 10	Length 405
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Db	1	ATGGGATGGAGCTGGATCTTCTCTCCCTCGTCAGAGACTGCAGGGGCTCCACTCTGAG	60	
OY	61	gtccagctgtgtgcagctctgtgggctgaagtgaagaacctggagctcagctgaagtgctc	120	
Db	61	GTCCAGCTTTCACACACTCAGGAGACTGAGCTGGGGAACCTGGGGCCCTCAGTGAAGATATCC	120	
OY	121	tgcgaagcttcgcgttaacaacttaactgaatgctatagaagtggtgtgaagcagctcct	180	
Db	121	TCGCAAGCCTTCGTGATACACTTCACACTGCATCAACATGCACTGGGTGAAGCAGCCAT	180	
OY	181	ggacagggagcctcagctgtgaatctgaatctaatatctactatgaataataacaactacaac	240	
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Db	241	CAGAAGTTCAAGAGCAGAGCCACATTGACTGTAGACAAATTCCTCCAGCACACAGCTAACATG	300	
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Db	301	GACGTCCGAGCCTGACATCTTGAGGACTGTGAGTCTATTTACTGTGCAAGAGGAGCGCCC	360	
OY	361	tatatgactactgtgtgtcaaggtacacctgtgcacgctctctca	405	
Db	361	GCTATGACTACTGGGGTCAAGAACTCAGTCACCGTCTCTCA	405	
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LOCUS	178617	405 bp	DNA	03-APR-1998
DEFINITION	Sequence 68 from patent US 5693762.			
ACCESSION	178617			
VERSION	178617.1	GI:3014771		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 405)			
AUTHORS	Queen, C.L., Co, M. Sung, Schneider, W.P., Landolfi, N.F., Coelingh, K.L. and Selick, H.E.			
TITLE	Humanized immunoglobulins			
JOURNAL	Patent: US 5693762-A 68 02-DEC-1997;			
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Best Local Similarity	75.3%	Pred. No. 2.2e-66		
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QY	61	gtccagctggtgacatctctgggctctgaggtgaagaagcctgggagctcagctgaaggtgtcc	120
Dd	61	GTCCAGCTTTCAGACGACTCAGAACCTGAGCTGGTGAAGAACTGGGGCCCTCAGTGAAGATATCC	120
QY	121	tgcacagcttcgcgcgtacacatctcactgatatgtctaacagttgggtgaagaagctctct	180
Dd	121	TGCAAGGCTTCTGGTGAACACATCTCACTGACATCAACAACATGACACTGGGTGAAGCAGCCAT	180
QY	181	ggacagggccctcgaatggatctgaagttatataatctactgataatacaaacacaaac	240
Dd	181	GGAAAGACCTTGATGGATGGATTTGGATATATTTATCTTTACATAGTGTGGTACTAGCTTACAC	240
QY	241	cagaagttlaagggcacaagccacaatgaactgctgtagaagaagctcgacagacagactatag	300
Dd	241	CAGAAGTTCAAGAGACCAAGGCCACATTGACTGATGACAAATTCCTCCAGCAGACCTTACATG	300
QY	301	gaacttagctcttgagttctgagatgacagccgtttctactgtcagaagcgccctgg	360
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QY	361	tataatgactactggtggcgaaggtacccctgtcacagctctccca	405
Dd	361	GCTATGAGACTACTGGGGTCAAGGAACGTCAGTACACGCTCTCCTCA	405
RESULT	10		
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DEFINITION	HSBUD114H	405 bp mRNA	PRI
LOCUS	Homo sapiens mRNA for anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b).		27-OCT-1994
ACCESSION	Z46348		
VERSION	Z46348.1	GI:560839	
KEYWORDS	anti-Sm antibody; diversity region; immunoglobulin heavy chain; joining region; variable region.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryote: Metazoa: Chordata: Vertebrata; Mammalia: Eutheria; Primates: Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 405)		
JOURNAL	Mahmoudi, M., Edwards, J., Cairns, E. and Bell, D.		
REFERENCE	Molecular characterization of natural human anti-Sm autoantibodies unpublished		
AUTHORS	2 (bases 1 to 405)		
TITLE	Mahmoudi, M.		
JOURNAL	Direct Submission		
FEATURES	Submitted (24-OCT-1994) Mahmoudi M., University of Western Ontario, Medicine and Microbiology and Immunology, University Hospital Room BRE-12, London, Ontario, Canada, N6A 5A5		
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	/db_xref="GI:560840"		
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PR      01-APR-1996 JP 96P   78570
PI      SERTIZAWA NOBUKI, NAKAHARA KAOI, ICHIKAWA KIMIHISA, PI
YONEHARA SHIN
PC      C12P21/08.C07K21/04.C07K16/28.C12N1/21.C12N15/09, PC
C12P21/02//A61K39/395,
PC      A61K39/395.G01N33/531.G01N33/577.(C12P21/08.C12R1/19), PC
(C12N1/21.C12R1/19).
PC      C12P21/02.C12R1/19);
CC      Strandedness: Double;
CC      Topology: Linear;
FH      Location/Qualifiers.
FH      key
FH      source
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FT      /cell-type='hybridoma'
FT      /cell-line='CH11'
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FT      anti-human Fas
FT      mouse monoclonal antibody CH11' FT
S1G-peptide 1..57
FT      V_region 58..405
FT      misc_feature 406..1770
FT      /product='constant region'.
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location/Qualifiers
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/db_xref='taxon:10090'
BASE COUNT .
ORIGIN
454 a 513 c 417 g 389 t
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Db 361 GCTGCTATTTTGACTACTGGGGCCAGGGAACCCGTGTACACCGTCTCTCA 411

	RESULT	15
MUSANTVDJ		
LOCUS		
DEFINITION	MUSANTI-DNA autoantibody variable region, diversity region, and joining region.	
ACCESSION	M37621	
VERSION	M37621.1	
KEYWORDS	GI:293302	
SOURCE	D-region; J-region; V-region; anti-DNA autoantibody.	
ORGANISM	Mus musculus (strain BALB/c, sub-species domesticus) DNA.	
REFERENCE	1 (bases 1 to 451)	
AUTHORS	Kofler, R., Noonan, D.J., Levy, D.E., Wilson, M.C., Moller, N.P., Dixon, F.J., and Theofilopoulos, A.N.	
TITLE	Genetic elements used for a murine lupus anti-DNA autoantibody are closely related to those for antibodies to exogenous antigens	
JOURNAL	J Exp. Med. 161 (4), 805-815 (1985)	
MEDLINE	85159423	
FEATURES	Location/Qualifiers	

Query Match	59.7%	Score 241.8	DB 94	Length 451
Best Local Similarity	74.8%	Pred. No. 2.3e-65		
Matches 303; Conservative	0	Mismatches 102	Indels 0	Gaps 0

OY	1	atggattggaaactatcatcattctcttcglttaccaacaactaaagtgagactccag	60
Db	47	ATGGGATGGAACTATCATCTCTCTTTTGGTAGCAGCACTACAGGTGTCCACTCCAG	106
OY	61	gtccagctcgtgcagctctcgaggtcgaaagtcgaagaagccctggagctcaagtgaagtgcc	120
Db	107	GTCCACTGCAGCAGACGCTGTGTCTGACCTTGTGAAGCTTGGGGCTTATGTMAAGCTGCC	166
OY	121	tgcagaagcttcgagctcaacacattcaactgatatgctatacagaagtggtgagacagctcct	180
Db	167	TGCAGAAGCTTCTGCAGCTACACTTTTCACCAGCACTAGATMAAACTGGTGAAGCAGAGCCT	226
OY	181	ggacagagggccctcgaggtgattggaggttatataatttacctatgatataaacactaaac	240
Db	227	GGACAAAGGCTTGTAGTGGATTGGAATTAATTTATCTCTGGTAGTAATACTTAATAAT	286
OY	241	cagaagtttaagggcaagagccacaatbactgtagaagaagtgcagcgacagccctatag	300
Db	287	GAGAAAGTTCAAGAGCAAGGCCACACTGACTGTAAACACATCTCCACACACAGCCTACATG	346
OY	301	gaacttagtctcttgaatatctgaagatacggcgcttattactagcttgcaagaagcggcctgg	360
Db	347	CAGCTCACACACCTGACATCTGCAGCACTCTCGGTATATTATGTGCAAGATGTGTGA	406
OY	361	tatatgaaactcgtgggttcaaggttaacctgtgtacacgctctcccta	405
Db	407	GGGTTTGCTTACTGGGGCCAGGACACTGTGTCACTCTCTGTGCA	451

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 29, 2001, 18:58:13 ; Search time 1635.84 Seconds
(without alignments)
36.187 Million cell updates/sec

Title: US-09-249-011-5
Perfect score: 405
Sequence: 1 atgggttggaactgtatcat.....ccctgtcacgcgtcctcta 405

Scoring table: IDENTITY_MNC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 73081774 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

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2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
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 233: em_gss_vrt36:*
 234: em_gss_vrt37:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	233.8	57.7	771	144	BF140551 601787584
2	232	57.3	724	144	BF168514 601775412
3	230.4	56.9	769	144	BF168556 601775314
4	226.6	56.0	488	114	AM403591 UI-HF-BKO
5	226.6	56.0	764	150	BF580556 602097359
6	226	55.8	911	165	BE286958 601092470
7	225.6	55.7	847	144	BF165486 601777393
8	224.4	55.4	567	165	BE287568 601097304
9	224.2	55.4	739	165	BE284158 601099428
10	224.2	55.4	1093	171	BF974290 602243946
11	224	55.3	417	115	AM408371 UI-HF-BKO
12	223	55.1	889	144	BF134160 601778840
13	220.8	54.5	477	171	BF975791 602246355
14	220.8	54.5	488	102	AI791363 oh68a09.Y
15	220.8	54.5	494	172	BC060202 nah49q10.
16	220.8	54.5	698	150	BF584024 602096264
17	220.8	54.5	849	150	BF582051 602099230
18	220.8	54.5	1012	171	BF974633 602243363

19	220.2	54.4	950	169	BF788670	602105561
20	220	54.3	513	114	AM402081	UI-HF-BK0
21	219.8	54.3	516	114	AM402422	UI-HF-BK0
22	218.8	54.0	477	115	AM408484	UI-HF-BK0
23	218.2	53.9	567	114	AM403728	UI-HF-BK0
24	218	53.8	684	150	BF577847	602092155
25	217.8	53.8	748	144	BF136397	601783927
26	216.4	53.4	592	145	BF238102	601811822
27	216.2	53.4	700	149	BF540088	602050325
28	215.6	53.2	510	114	AM403806	UI-HF-BK0
29	215.2	53.1	498	114	AM402294	UI-HF-BK0
30	215	53.1	449	114	AM402364	UI-HF-BK0
31	215	53.1	507	142	BF015548	uy23a08.Y
32	215	53.1	864	151	BF663151	602145073
33	214.4	52.9	527	114	AM402139	UI-HF-BK0
34	214.2	52.9	379	121	AM908776	UI-HF-BK0
35	214	52.8	473	165	BE307170	601098164
36	213.4	52.7	517	149	BF545108	UI-R-C2D-
37	213	52.6	485	114	AM403940	UI-HF-BK0
38	212.6	52.5	438	118	AM630198	60179907.Y
39	212.4	52.4	517	115	AM408270	UI-HF-BK0
40	212.4	52.4	934	144	BF139595	601785525
41	212.2	52.4	1018	151	BF663940	602145606
42	211.8	52.3	542	114	AM405977	UI-HF-BK0
43	211.6	52.2	406	142	BF016722	uy34h12.Y
44	211.6	52.2	419	114	AM402189	UI-HF-BK0
45	211.2	52.1	1012	150	BF579009	602096127

ALIGNMENTS

RESULT 1
LOCUS BF140551 771 bp mRNA
DEFINITION 601787584F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4015172 5',
mRNA sequence.
ACCESSION BF140551
VERSION BF140551.1 GI:10979591
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 771)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LHAM9260 row: h column: 21
High quality sequence stop: 648.

FEATURES

source 1..771
Location/Qualifiers
/organism="Mus musculus"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:4015172"
/clone_1id="NCI_CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH108"
/note="Organ: Lung; Vector: pCMV-SPORT6; Site_1: NCI;
Site_2: Salt; transgenic model WM-1; expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies."

BASE COUNT 179 a 215 c 195 g 182 t
ORIGIN
Investigator providing samples: Gilbert Smith, NIH"

Query Match 57.7%; Score 233.8; DB 144; Length 771;

Best Local Similarity 73.6%; Pred. No. 3.8e-60;

Matches 298; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

Oy	1	atgggttggaactatcatcttcttcttggtttaccacagctacagtgatgacactccag	60
Db	15	ATGGAGTGGGCTGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	74
Oy	61	gtccagcggcgagcggcgtcggcgagtggaagccttggaagcctgaagtgatgac	120
Db	75	GTTGAGTTGAAGCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG	134
Oy	121	tgcgaagcttcggcgtacacatcactgatatgctatgacagtggtgagcaagcctc	180
Db	135	TGCAAGGCTTCTGGCTACACCTTCAACAGCTATATTATGCACTGGGTGAAGCAGGCT	194
Oy	181	ggacaaggcctcggatgagtgatgagttataataattactatgataaacactaac	240
Db	195	GGACAGGCGCTTGAGTGAGTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	254
Oy	241	cagaagtttaaggcgaagcgaagcgaagcgaagcgaagcgaagcgaagcgaagcga	300
Db	255	GAGAGTTCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	314
Oy	301	gaacttagttcttgaagctcgaagcgaagcgaagcgaagcgaagcgaagcgaagcga	360
Db	315	GAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	374
Oy	361	tatatgaactactgggtcgaagtgacacctgtcacgcgtctcccta	405
Db	375	GTAATTGACTACTGGGGCAGGACGACCATATCACTACAGTCTCTCA	419

RESULT 2
LOCUS BF168514 724 bp mRNA
DEFINITION 601775412F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:4017075 5',
mRNA sequence.
ACCESSION BF168514
VERSION BF168514.1 GI:11048866
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 724)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LHAM9265 row: h column: 04
High quality sequence stop: 661.

FEATURES

source 1..724
Location/Qualifiers
/organism="Mus musculus"
/strain="CZECH II (fetal)"
/db_xref="taxon:10090"
/clone="IMAGE:4017075"
/clone_1id="NCI_CGAP_Lu29"

DNA Sequencing by: M.B. Soares lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/dbp/image/image.html
Seq primer: M13 Forward.

BASE COUNT ORIGIN	111 a	136 c	140 g	101 t

Query Match	56.0%	Score 226.6	DB 114	Length 488
Best Local Similarity	73.5%	Pred. No. 5.1e-58		
Matches 311	Conservative 0	Mismatches 94	Indels 18	Gaps 1

[illegible]

Oy	181	ggacaggccctcagatggatggaggttaataattacctatgatataaacaactaac	240
Db	182	ggacaaaggcttgatggtgatggatggatcaacgcttgcaattgtatcaccaaatattcca	241
Oy	241	cagaagtttaaggccaagccacacatgactgttagacaagtcgacagacagcctatag	300
Db	242	cagaagtttcaggccacagtcaccattggccacaggacacacattcccgacacacagcctcatc	301

OY	301	gaacttagctctcttgagatactgagataacgagccgttattacccgtgcaagacgc	-----	354
Db	302	gagcttgagcagccctgagatgctggaacacacgctgtgtattactgtggagacggcggaatt		361
OY	355	-----gcctggtatattgactactgggtgtcaaggtacacctgtgacacgctctcc		402
Db	362	tactatgcttcaggagagcttcttcttgactactcggggccagggaaacccgtgacccgctctcc		421
OY	403	tca	405	
Db	422	tca	424	

RESULT	5				
LOCUS	BF580556				
DEFINITION	BF580556 60209735959.1 NCI_CGAP_C024 Mus musculus cDNA clone IMAGE:4217102 5'	764 bp	mRNA	EST	12-DEC-2000
ACCESSION	BF580556				
VERSION	BF580556.1	GI:11654268			
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
	Eumetazoa; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				

REFERENCE	1 (bases 1 to 764)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

BASE COUNT	194 a	198 c	195 g	177 t
ORIGIN				

Query Match	56.0%;	Score 226.6;	DB 150;	Length 764;
Best Local Similarity	- 74.1%;	Pred. No. 5.8e-58;		
Matches 300; Conservative	0;	Mismatches 104;	Indels 1;	Gaps 1

QY	61	gttgcagctcgtggtcagctctcgtgggctcgaagtcgtgaagaagcctctgagcgtcaatgaaagctctcc	120
Db	97	gttcacactgcacacacacctctgggctcttgcctgctgaagccttgagccttcagttanactgtcc	155
QY	121	tgcagaagcttcgcgtacacactcactgatatcgtctatacagctgggtgtgagacagcgtcctc	180
Db	157	tgcacagcgtcttctggctacacattccacgcgtactcggatcgaatgcactctgggtgacacacagggcctt	210

QY	161	ggaacggagcctcogatgtagtattggaagttataataatlttactatgataaacaaactaac	24
Db	217	ggacaaagcccttgaotgsa-tggaaagacattatccctactagtgcagagaccacactacgat	275
QY	241	cagaagtttaaggggcaagggccacaatgactctttagaacaagttcgacgagacacagcctat	30
Db	276	gagaaattcaaggggcaagggccacactgactcttagacacatcctccagacagccctacgtg	333
QY	301	gaactagttcttcagatctgagatcacggcgtttatctactctgcaagaggggccttg	36
Db	336	gattttcacacagcctgacactctgagagactcacagggtcttattttgtaacaaagagagggaaa	39

Qy 361 tatatgactactggtgtcaaggtacccttgtcaacgctctctca 405
| | | | | | | | | | | | | | | | | | | | | |
Db 396 GAGTTTGACTACTGGGCCAAGGCACCACTCTCATAGTCTCCTCA 440

Db	396	GAGTTTGACTACTGGGCGCCAAAGCACCACCTCTCATATGTCTCTCA	440
RESULT	6		
BE286958			
LOCUS			
DEFINITION	BE286958	911 bp	mRNA
	601092470P1	NCI_CGAP_Mam5 Mus musculus	CDNA clone IMAGE:3487241 5'
ACCESSION			
VERSION	BE286958		
KEYWORDS	EST.	BE286958.1	GI:9165654

SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 911)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Lohar Hemigausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM524 row: k column: 18
High quality sequence stop: 688.
Location/Qualifiers
1. 911
/organism="Mus musculus"
/strain="C57/B6"
/db_xref="taxon:10090"
/clone_1lb="IMAGE:3487241"
/clone_1lb="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: PCMV-SPORT6; Site:1: Salt; Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lohar Hemigausen/Robin Humphreys, NIH"

BASE COUNT 190 a 262 c 261 g 197 t 1 others
ORIGIN

Query Match 55.8%; Score 226; DB 165; Length 911;
Best Local Similarity 75.2%; Pred. No. 9.3e-58;
Matches 310; Conservative 0; Mismatches 95; Indels 7; Gaps 2;

QY 1 atgggttggaactgtatcattcttcttctgttaccacagctacaggtgtgactccag 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 8 ATGGGATGGAGCTGTATCATGCTCTCTCTGGCAGCAGCTACAGGTGCCACTCCAG 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 gtccagctgtgtcagctgtgggctggaagctggaagctggaagctggaagctgctc 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 68 GTCCAACTGCAGAGCCTGGGGCTGAGCTGTGTAAGCCTGGGCTTCAGTAAAGCTGTC 127
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 tgcagaagcttcgcgctacacattcaactgattatgctatagctgtgtg-agaacagctcc 179
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 128 TGCAGAGCTTCTGTGCTACCTTACCACTTACGATGACACTGGGTGAACGACAGGCC 187
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 180 tgcagcaggcctcgaagtgtgattgattatataattactactatgataataacatacaa 239
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 188 TGCAGAGCCTTGTGAGTGTGTAAGAGTGTGATCTAATAGTGTGCTACTAGTACAA 247
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 240 ccagaatttcaaggaagcacaatgactgtatgacaagtgcagcagcagaagctatat 299
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 248 TGAAGATTCAAGAGCAAGGCCACACTGACTGTAGACAAACCCCTCCAGCAGCTACAT 307
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 300 ggaacttagttcttggatctgaggaataagcgcgttattactgttcaagaagcgcctg 359
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DB 308 GCAGCTCAGCAGCCTGCATCTGAGACTCTGCGGTCTATTACTGTACAGAGGGGGA 367
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QY 360 gta-----tatggaactactgtgggtcaaggtacacctgttcaacgcttcccta 405
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DB 368 TTACGAGCGTATGAGCTAGTGGGTCAAGGAAGCTCAGTACCGCTTCCTCA 419
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RESULT 7*

BF165486
LOCUS BF165486 847 bp mRNA
DEFINITION 601777393F1 NCL_CGAP_Lu29 Mus musculus cDNA clone IMAGE:4019039 5', mRNA sequence.
ACCESSION BF165486
VERSION BF165486.1 GI:11045851
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 847)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM9270 row: i column: 24
High quality sequence stop: 760.
Location/Qualifiers
1. 847
/organism="Mus musculus"
/strain="CZBCH II (fetal)"
/db_xref="taxon:10090"
/clone_1lb="IMAGE:4019039"
/clone_1lb="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary. Stem cell origin."
/lab_host="DH10B"
/note="Organ: lung; Vector: PCMV-SPORT6; Site:1: Salt; Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Gilbert Smith, NIH"

BASE COUNT 179 a 223 c 242 g 203 t
ORIGIN

Query Match 55.7%; Score 225.6; DB 144; Length 847;
Best Local Similarity 73.8%; Pred. No. 1.2e-57;
Matches 301; Conservative 0; Mismatches 104; Indels 3; Gaps 1;

QY 1 atgggttggaactgtatcattcttcttctgttaccacagctacaggtgtgactccag 60
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DB 14 ATGGGATGGGCGCTGGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 73
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QY 61 gtccagctgtgtcagctgtgggctggaagctggaagctggaagctggaagctgctc 120
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DB 74 GTTCAATTGAAGCGTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCT 133
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 tgcagaagcttcgcgctacacattcaactgattatgctatagctgtgtgatacagaagctcc 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 124 TGCAGAGCTTCTGTGCTACCTTACCACTATATTATGCACTGGGTGAACGACAGGCT 193
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 134 TGCAGAGCTTCTGTGCTACCTTACCACTATATTATGCACTGGGTGAACGACAGGCT 193
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 ggaacggcctcgaagtgtgattgattatataattactactatgataataacatacaac 240
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 194 GGACAGGGCCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 253
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 cagaagtttaagggcagaagccacaatgactgtatgacaagctgcagcagaagcctatat 300
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DB 254 GAGAAGTTCAAGAGCAAGGCCACACTGACTGTACCAAAATCTTCACACAGCCTACATG 313
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QY 301 gaacttagttcttggatctgaggaataagcgcgttattactgttcaagaagcgcctg 360
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 314 GAGCTCAGCAGCCTGACCTGTGAGGACTGTGCGCTATTACTGTGCAAGGAGCTACAGT 373
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Qy 361 tata---tgcactactgggtcaaggtacccctgtcacgcgtcccca 405
 Db 374 gttacgcttgactactggggcccaagcaccactatcacagctctcccca 421

RESULT 8

LOCUS BE287568 567 bp mRNA EST 26-OCT-2000
 DEFINITION 601097304F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3495985 5',
 mRNA sequence.

ACCESSION BE287568.1 GI:9166664

VERSION BE287568.1

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

Plate: LLM8547 row: h column: 02

High quality sequence stop: 563.

Location/Qualifiers

FEATURES

Source

1..567

/organism="Mus musculus"

/strain="C57/B6"

/db_xref="taxon:10090"

/clone="IMAGE:3495985"

/clone_lib="NCI_CGAP_Mam5"

/tissue_type="tumor, gross tissue"

/dev_stage="7 months"

/lab_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI;

Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Library constructed by Life Technologies. Investigators

providing samples: Lothar Hennighausen/Robin Humphreys,

NIH"

BASE COUNT 137 a 152 c 147 g 131 t

ORIGIN

Query Match 55.4%; Score 224.4; DB 165; Length 567;
 Best Local Similarity 73.4%; Pred. No. 2.5e-57;

Matches 304; Conservative 0; Mismatches 101; Indels 9; Gaps 1;

Qy 1 atgggttggaactgtatcatctcttcttggttaccaagcagtggtgaccccg 60

Db 17 ATGGGATGAGCTCTATCATCTCTTCTTGAGCAACAGCTACAGGTCTCCAG 76

Qy 61 gtccagctggtgcagctcgtgagctgagtgaaagccctggagcagctgaagtgtcc 120

Db 77 GTCCAACTGCACAGCCTGCGGCTGAGCTGCTGAGGCTCGGAGTTTCATGAAGCTGTC 136

Qy 121 tgcagaactccggtacacatcattgattatgctatacagtggtgagacagctcct 180

Db 137 TGCAGAGCTTCTGCTACCTCTTCAACCGACTACTGGGTGAACCTGGGTGAAGCAGAGGCT 196

Qy 181 ggaagggccctcagtgatgattgagttatataattactatgataatacaaacacac 240

Db 197 GGACAGGCTTGTGAGTGGATGATGATTCCTCCGATGAGTGAATTTAGTTAAAT 256

Qy 241 cagaagtttaagggcaagccacaatgactctagacaagtcgacagacacagctatag 300

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 Db 257 CAGAGTTTAAGCAAGAGCCACATTGACTGTAGCAAAATCTCCAGCAGACCTATCATG 316

Qy 301 gaactagtctcttgagatcagaataagccgtttatctactgtgcaagagcgctcg 360

Db 317 CAACTCAGAGCCCGCAGCATCTGAGAGCTGCTATTTACTGTGCAAGAGCAGCGC 376

Qy 361 tatatgac-----tactgggtcaaggtacacctgtcacgcgtcccca 405

Db 377 TACGTAGACTGGTTATTATTATTGGGCCAAGGAGACTCTGTCTCTGTCA 430

RESULT 9

LOCUS BE284158 739 bp mRNA EST 13-JUL-2000

DEFINITION 601099428F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3491766 5',
 mRNA sequence.

ACCESSION BE284158

VERSION BE284158.1 GI:9160900

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

Plate: LLM8536 row: h column: 07

High quality sequence stop: 535.

Location/Qualifiers

1..739

/organism="Mus musculus"

/strain="C57BL/6J (f1)"

/db_xref="taxon:10090"

/clone="IMAGE:3491766"

/clone_lib="NCI_CGAP_Lu29"

/tissue_type="spontaneous tumor, metastatic to mammary.

stem cell origin."

/lab_host="DH10B"

/note="Organ: lung; Vector: pCMV-SPORT6; Site:1: SalI;

Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Library constructed by Life Technologies. Investigators

providing samples: Gilbert Smith, NIH"

BASE COUNT 184 a 210 c 184 g 161 t

ORIGIN

Query Match 55.4%; Score 224.2; DB 165; Length 739;
 Best Local Similarity 73.5%; Pred. No. 3.1e-57;

Matches 302; Conservative 0; Mismatches 103; Indels 6; Gaps 1;

Qy 1 atgggttggaactgtatcatctcttcttggttaccaagcagtggtgaccccg 60

Db 13 ATGGATGATCTGATGATCTTCTTCTTCATCTCTCAAGAGTCAAGTCTCCAG 72

Qy 61 gtccagctggtgcagctcgtgagctgagtgaaagccctggagcagctgaagtgtcc 120

Db 73 GTTCACTGCACAGCCTGAGCTGAGCTGCGGAGGCTCGGCTTCATGAAGATGTC 132

Qy 121 tgcagaactccggtacacatcattgattatgctatacagtggtgagacagctcct 180

Db 133 TGCAGGCTTGTGATGATTCATCAACAGCTATGATTAAGTGGGTGAAGCAAAACT 192

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Oy 181 ggaaggggagcctcgaatggatggatcttaattactactatgataatcacaaacacac 240
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Db 193 AGACAGGGCCTTGATGGATTTGGACAGATTTATCTCGAAGAGGGTAACACTTACTACAT 252
Oy 241 cagaagcttaagagggaagcccaatgactctgagacaagtcgaagcagcacgacctatg 300
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Db 253 GAAAGGTTCAAGGCGAAGGCCACACTGACTGCAGACAAATCTCCAGACACACGCTACATG 312
Oy 301 gaacttagtctctttagatctctgagatacggccgttacttactgtcgaaga-----gcg 354
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 313 CAGCTCAGACAGCCTGACATCTGAGACCTCTGAGACTCTATTCTGTGCAAGATGGGGGAG 372
Oy 355 gctctgatatagactactgtgggttaagtgatccctgttcacgcttctctca 405
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 373 CCTTGGAAGCTGGACTACTGGGGCCAAAGCACACACTATACAGTCTCCTCA 423

RESULT 10
LOCUS BP974290 1093 bp mRNA EST 22-JAN-2001
DEFINITION 602243946p1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4335131 5',
mRNA sequence.
ACCESSION BP974290
VERSION BP974290.1 GI:12341505
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1093)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM1205 row: 1 column: 12
High quality sequence stop: 759.
Location/Qualifiers
1..1093
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4335131"
/culture="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pCMV8; Site: 1: XhoI;
Site: 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Size selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC Library."
BASE COUNT 281 a 330 c 299 g 183 t
ORIGIN

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Query Match      55.4%:  Score 224.2:  DB 171:  Length 1093:
Best Local Similarity 73.5%:
Matches 302:  Conservative 0:  Mismatches 103:  Indels 6:  Gaps 1:

0y      1  atgggttggaactgcatcatctctcttcgtgtaccacagctacagcgtgcacccag 60
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Db	41	ATGACCTGCACCTGGAGGATCTCGTCTTGTTGGCAGAGACTACAGGCACCCAGGCCAG	100
OY	61	gtccagctgtgtgcagctcttggggtctgaagtgaaagccctggagctcaagtgaagtgctc	120
Db	101	GTCCAGCTGTGATCAGTCTGGGGCTTGAGGTGAAGAAGCTTGGGGCTTACGTAAAGTCTCC	160
OY	121	tgcagaagcttcggtgtacacattcaactgatatgtcctaagaatgggtggaacagggctcc	180
Db	161	TCCAAGGTTTCCGGCTTACACCTTACTCAATTAATTCATATGCACTGGGTGCACAGGGCTCT	220
OY	181	ggacagggccctcgatgtgattgagatcttaatacttaactatgaataaacaattacaac	240
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OY	241	cagaagcttlaagggcaagggcacacaatgactgttagacaagtcagcagcgacaagcctatg	300
Db	281	CAGAGTTCACGGGGAGAGTCAACCATGACCGAGGACACATCTACAGACGCGCTTACATG	340
OY	301	gaacttagtctcttgagatcttgagatacgggcgtttatactactgtgcaa-----gagcg	354
Db	341	GAGCTGACACAGCTCAGATTCAGACGACACGGGCGCTGTATTAAGTGTGCACACTTACCATGAT	400
OY	355	gccttgatatatgahattacttggggccaagtaacctgtgaecgctctctca	405
Db	401	ATTAGGGCTCTGACTTACTTGAGGCCAGGAACCTGTGGACCGTCTCTCA	451

RESULT	11			
LOCUS	AM408371			
DEFINITION	AM408371	417 bp	mRNA	EST
ACCESSION	U1-HF-BK0-ab1-c-03-0-UI.t1.NH.MGC_36			16-FEB-2000
VERSION	IMAGE:3056620 5,			sapiens cDNA clone
KEYWORDS	AM408371			
SOURCE	AM408371.1	GI:6927428		
ORGANISM	EST.			
REFERENCE	human.			
AUTHORS	Homo sapiens/			
TITLE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi,			
COMMENT	Mammalia: Eutheria: Primates: Catarrhini: Hominiidae: Homo.			
	1 (bases 1 to 417)			
	NIH-MGC http://mgc.nci.nih.gov/ .			
	National Institutes of Health, Mammalian Gene Collection (MGC)			
	Unpublished (1999)			
	Contact: Robert Strausberg, Ph.D.			
	Tel: (301) 496-1550			
	Email: Robert.Strausberg@nih.gov			
	EST RI site shown at the beginning of the sequence.			
	Tissue Procurement: Louis M. Straud, M.D., Ph.D.			
	CDNA Library Preparation: M.B. Soares Lab			
	CDNA Library Arrayed by: M.B. Soares Lab			
	DNA Sequencing by: M.B. Soares Lab			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LLNL at:			
	www-bio.llnl.gov/brp/image/image.html			
	Seq primer: M13 forward.			

FEATURES	SOURCE
Location/Qualifiers	1. 1417
/organism="Homo sapiens"	
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/clone_IMAGE:3056620"	
/clone_1b="NH_MGC_36"	
/tissue_type="Lymph"	
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/cell_line="MGC85"	
/lab_host="DH10B (LTI)"	
/note="Vector: pRT3-Pac; Site_1: NotI; Site_2: Eco RI;	
Constructed from size fractionated cytoplasmic mRNA	
(0.5-1.5kb). Directionally cloned. Cells provided by Louis	
M. Staudt, Ph.D. Library preparation by Maria de Fatima	
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."	
BASE COUNT	91 a 106 c 130 g 90 t
ORIGIN	

JOURNAL
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
unknown library type
Seq primer: -40RP from GIBCO
High quality sequence stop: 425.

FEATURES
Location/Qualifiers
1..494

BASE COUNT 132 a 123 c 143 g 96 t
ORIGIN
Query Match 54.5%; Score 220.8; DB 172; Length 494;
Best Local Similarity 76.7%; Pred. No. 2.9e-56;
Matches 270; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4254907"
/clone_lib="NCI CGAP_HN19"
/tissue_type="normal epithelium"
/lab_host="DH10B"
/note="Organ: nasopharynx; Vector: pAMP10; mRNA made from normal nasopharyngeal epithelium, cDNA made by oligo-dT priming. Non-directionally cloned into UDG sites. Size-selected on agarose gel, average insert size 500 bp. Primary library. cDNA library preparation: David B. Krizman, Ph.D. REFERENCE: Krizman et al. (1996) Cancer Research 56:5380-5383."

Query Match 54.5%; Score 220.8; DB 172; Length 494;
Best Local Similarity 76.7%; Pred. No. 2.9e-56;
Matches 270; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
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61 gtccagctgtgcaagctctgaggctgaagaaagcctgggagctcagtgaaagtgcc 120
Db 93 GTCCAGCTGTGACAGCTGGGGCTGAGGGAAGAGCCTGGGGCCTCAGTGAAGGTCTCC 152
121 tgcgaagcttcgcgtacacattcaatgatactatacagtgaggtagacaggtcct 180
Db 153 TGCAGGTTTCCGAGTACACCTCCTACATGATTCATGCACTGGGTGCGACAGGCTCCT 212
181 ggcagaggtcgcagtgagtgatgagttatattactatgataataaactacaac 240
Db 213 GGAAGAAGGCTTGAAGTGGAGGTTTGTATCTGAAGATGCTGAACAATCTTACGCA 272
241 cagaagtttaagggcaagccacaaatgactgtagacaagtcgacgagcagcctatag 300
Db 273 CAGAAGTTCAGAGGCGAGAGTACACATGACCGAGACACATCTACAGACACACCTACATG 332
301 gaactagttcttgagatctgagatcagcgcgttattactctgtcaagag 352
Db 333 GAGCTGAGCAGCCTGAGATCTGAGACACAGCGCGGTGATTTACTGTGCAACAG 384

Search completed: April 29, 2001, 20:11:00
Job time: 4367 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 29, 2001, 19:41:33 ; Search time 151.39 Seconds
(without alignments)
1561.737 Million cell updates/sec

Title: US-09-249-011-5

Perfect score: 405
Sequence: 1 atgggttgacgtatcatc.....ccctgtcacgcgtctctca 405

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: N.Geneseq_0401: *
2: /SID2/gcgdata/geneseq/geneseq/NA1980.DAT: *
3: /SID2/gcgdata/geneseq/geneseq/NA1981.DAT: *
4: /SID2/gcgdata/geneseq/geneseq/NA1982.DAT: *
5: /SID2/gcgdata/geneseq/geneseq/NA1983.DAT: *
6: /SID2/gcgdata/geneseq/geneseq/NA1984.DAT: *
7: /SID2/gcgdata/geneseq/geneseq/NA1985.DAT: *
8: /SID2/gcgdata/geneseq/geneseq/NA1986.DAT: *
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10: /SID2/gcgdata/geneseq/geneseq/NA1988.DAT: *
11: /SID2/gcgdata/geneseq/geneseq/NA1989.DAT: *
12: /SID2/gcgdata/geneseq/geneseq/NA1990.DAT: *
13: /SID2/gcgdata/geneseq/geneseq/NA1991.DAT: *
14: /SID2/gcgdata/geneseq/geneseq/NA1992.DAT: *
15: /SID2/gcgdata/geneseq/geneseq/NA1993.DAT: *
16: /SID2/gcgdata/geneseq/geneseq/NA1994.DAT: *
17: /SID2/gcgdata/geneseq/geneseq/NA1995.DAT: *
18: /SID2/gcgdata/geneseq/geneseq/NA1996.DAT: *
19: /SID2/gcgdata/geneseq/geneseq/NA1997.DAT: *
20: /SID2/gcgdata/geneseq/geneseq/NA1998.DAT: *
21: /SID2/gcgdata/geneseq/geneseq/NA1999.DAT: *
22: /SID2/gcgdata/geneseq/geneseq/NA2000.DAT: *
23: /SID2/gcgdata/geneseq/geneseq/NA2001.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	405	100.0	405	21	A59694	DNA encoding heavy
2	334.6	82.6	405	21	A59692	Nucleotide sequence
3	277.2	68.4	524	12	Q14802	Encodes murine anti
4	277.2	68.4	524	12	Q14802	R6-5-D6 anti-ICAM-
5	272.2	67.2	446	11	005554	Sequence encoding
6	265.8	65.6	1767	19	V61363	Anti-human Fas hum
7	265.8	65.6	1767	21	A78271	Anti-human Fas hum
8	265.8	65.6	1768	19	V61364	Anti-human Fas hum
9	265.8	65.6	1768	21	A78272	Anti-human Fas hum
10	254.4	62.8	424	17	T42717	Humc3 VH coding se
11	253.6	62.6	451	15	066702	DRG-200 Humanized

12	253.6	62.6	2071	19	V70080	Anti-Fas humanised
13	253.6	62.6	2071	21	A72184	DNA encoding human
14	253.6	62.6	2071	21	A11622	Humanised HFE7A de
15	252	62.2	2073	21	A11644	Humanised anti-Fas
16	252	62.2	2073	21	A11645	Humanised anti-Fas
17	251.6	62.1	2073	21	D00905	Humanised antibody
18	250.4	61.8	2073	21	A11646	Humanised anti-Fas
19	248.8	61.4	457	19	V70104	Humanised anti-Fas
20	248.8	61.4	457	21	A72146	Humanised anti-Fas
21	248.8	61.4	457	21	A11584	Humanised anti-Fas
22	248.8	61.4	2077	19	V70079	Humanised anti-Fas
23	248.8	61.4	2077	21	A72159	DNA encoding human
24	248.8	61.4	2077	21	A11597	Humanised HFE7A de
25	248.2	61.3	405	21	A59698	DNA encoding heavy
26	245.6	60.6	2077	21	A11655	Humanised anti-Fas
27	245.2	60.5	423	21	D00907	Humanised antibody
28	245	60.5	405	20	V33947	Humanised antibody
29	245	60.5	411	21	A48845	CDNA encoding huma
30	244.8	60.4	409	21	287738	Anti-human VEGF re
31	243.4	60.1	405	19	V37264	CDNA encoding a va
32	243.4	60.1	405	21	295282	CDNA encoding anti
33	243.4	60.1	1773	18	T88869	IgM chimeric antib
34	243.4	60.1	1773	19	V66735	H chain subunit of
35	243.4	60.1	1773	21	A78202	Anti-human VEGF re
36	242.2	59.8	478	20	V88433	Anti-human Fas ant
37	241.8	59.7	433	13	024790	EST clone GFI96.
38	240.8	59.5	421	18	T73624	Anti-Fas antibody
39	240.2	59.3	443	10	N91820	CDNA for humanised
40	240	59.3	409	21	287778	DNA sequence of th
41	239	59.0	418	19	V59116	Anti-human VEGF re
42	239	59.0	418	19	V07581	HML-24 antibody he
43	239	59.0	418	19	V07581	Anti-human HML-24
44	239	59.0	418	19	V39350	Humanised anti-HM1
45	239	59.0	418	19	V39357	Humanised anti-HM1

ALIGNMENTS

RESULT	1
ID	A59694 standard; DNA; 405 BP.
XX	
AC	A59694;
XX	
DT	14-NOV-2000 (first entry)
XX	
DE	DNA encoding heavy chain variable region of humanised 3S1 antibody.
XX	
KW	Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;
KW	autoimmune disease; infectious diseases; inflammatory disorder;
KW	systemic lupus erythematosus; diabetes mellitus; insulin; asthma;
KW	arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
KW	multiple sclerosis; transplant rejection; cancer; proliferative disease;
KW	leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
KW	aplastic anaemia; myeloid dysplasia syndrome; ss.
XX	
OS	Synthetic.
OS	Mus sp.
OS	Homo sapiens.
XX	
FT	Key
FT	CDS
FT	1..405
FT	/tag= a
FT	/product= "heavy chain variable region of 3D1 antibody"
FT	/note= "no termination codon given"
FT	1..57
FT	sig_peptide
FT	/tag= b
FT	mat_peptide
FT	58..405
FT	/tag= c
XX	
PN	WO200047625-A2.

PD 17-AUG-2000.
 XX 09-FEB-2000; 2000WO-US03303.
 XX 12-FEB-1999; 99US-0249011.
 PR 24-JUN-1999; 99US-0339596.
 XX (GEMV) GENETICS INST INC.
 PA
 XX Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;
 PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;
 XX WPI: 2000-524532/47.
 DR P-PSDB; B07965.
 XX Humanized immunoglobulin having a binding specificity to B7-1 (derived
 PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-1524) molecules,
 PT modulates immune responses and can therefore treat e.g. autoimmune
 PT diseases, infectious diseases -
 XX
 XX Example 3; Fig 2A; 162pp; English.
 PS
 XX The present sequence encodes the heavy chain variable region of the
 CC humanised murine antibody 3D1. The antibody has a binding specificity to
 CC B7 molecules. The antibody is used to construct humanized
 CC immunoglobulins, which comprise an antigen binding region of non-human
 CC origin and a portion of a human immunoglobulin. The humanized
 CC immunoglobulins are useful for treating autoimmune diseases, infectious
 CC diseases, inflammatory disorders, systemic lupus erythematosus, diabetes
 CC mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease,
 CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are
 CC also useful for treating a transplant recipient or preventing transplant
 CC rejection in a transplant recipient, and treating proliferative disease
 CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,
 CC thalassemia and aplastic anaemia), inborn errors of metabolism,
 CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
 CC
 XX Sequence 405 BP; 102 A; 88 C; 110 G; 105 T; 0 other;
 SO

Query Match 100.0%; Score 405; DB 21; Length 405;
 Best Local Similarity 100.0%; Pred. NO. 3.9e-102;
 Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgggttggaactgatatctctctctctgtgtaccacagctcaggtgtgactccag 60
 DB 1 atgggttggaactgatatctctctctctgtgtaccacagctcaggtgtgactccag 60
 QY 61 gtccagctgtgtcagctctgtgtgtgaggaagcctgtgagctcagtgaggtgtcc 120
 DB 61 gtccagctgtgtcagctctgtgtgtgaggaagcctgtgagctcagtgaggtgtcc 120
 QY 121 tgcagaagcttcgggtacacattcattatgtatcagtggtgtgagaagctcct 180
 DB 121 tgcagaagcttcgggtacacattcattatgtatcagtggtgtgagaagctcct 180
 QY 181 ggcagagggcctcgaagtggaattgaatttaattactatgaataacaacacacac 240
 DB 181 ggcagagggcctcgaagtggaattgaatttaattactatgaataacaacacacac 240
 QY 241 cagaagtttaaggcgaagccacaatgactgtagacaagtcgacgagcagccatata 300
 DB 241 cagaagtttaaggcgaagccacaatgactgtagacaagtcgacgagcagccatata 300
 QY 301 gaactattctttagtcttgagatagatagcggttattctgtgcaagagcggtcttg 360
 DB 301 gaactattctttagtcttgagatagatagcggttattctgtgcaagagcggtcttg 360
 QY 361 tatatgactactaggtgcaagtgacccctgtcacgcgtctctca 405
 DB 361 tatatgactactaggtgcaagtgacccctgtcacgcgtctctca 405

RESULT 2
 ID A59692 standard; DNA: 405 BP.
 AC A59692;
 XX 14-NOV-2000 (first entry)
 DE Nucleotide sequence of heavy chain variable region of 351 antibody.
 XX
 KW Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;
 KW autoimmune disease; infectious disease; inflammatory disorder;
 KW systemic lupus erythematosus; diabetes mellitus; insulinitis; asthma;
 KW arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
 KW multiple sclerosis; transplant rejection; proliferative disease;
 KW leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
 KW aplastic anaemia; myeloid dysplasia syndrome; ss.
 KW
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..405
 FT /*tag- a
 FT /product= "heavy chain variable region of 3D1 antibody"
 FT /note= "no termination codon given"
 FT sig_peptide 1..157
 FT /*tag- b
 FT mat_peptide 58..405
 FT /*tag- c
 FT
 XX WO200047625-A2.
 PN 17-AUG-2000.
 PD 09-FEB-2000; 2000WO-US03303.
 PR 12-FEB-1999; 99US-0249011.
 PR 24-JUN-1999; 99US-0339596.
 XX
 PA (GEMV) GENETICS INST INC.
 XX Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;
 PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;
 XX WPI: 2000-524532/47.
 DR P-PSDB; B07963.
 XX Humanized immunoglobulin having a binding specificity to B7-1 (derived
 PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-1524) molecules,
 PT modulates immune responses and can therefore treat e.g. autoimmune
 PT diseases, infectious diseases -
 XX
 XX Example 1; Fig 1A; 162pp; English.
 PS
 XX The present sequence encodes the heavy chain variable region of the
 CC murine antibody 3D1. The antibody has a binding specificity to B7
 CC molecules. The antibody is used to construct humanized immunoglobulins,
 CC which comprise an antigen binding region of non-human origin and a
 CC portion of a human immunoglobulin. The humanized immunoglobulins are
 CC useful for treating autoimmune diseases, infectious diseases,
 CC inflammatory disorders, systemic lupus erythematosus, diabetes
 CC mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease,
 CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are
 CC also useful for treating a transplant recipient or preventing transplant
 CC rejection in a transplant recipient, and treating proliferative disease
 CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,
 CC thalassemia and aplastic anaemia), inborn errors of metabolism,
 CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
 CC
 XX Sequence 405 BP; 110 A; 89 C; 102 G; 104 T; 0 other;
 SO

Query Match

82.6%; Score 334.6; DB 21; Length 405;

Best Local Similarity 89.1%; Pred. No. 8.2e-83;
Matches 361; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1 atgggttggaactgtatcatcttcttcttggttacacagctacaggtgtgacatccag 60
|||||
DB 1 atgggttggaactgtatcatcttcttcttggttacacagctacaggtgtgacatccag 60

QY 61 gtccagctgtgtcactgtcgtggtcgtgaggaagccgtggagctcaagtgaaggtgcc 120
|||||
DB 61 gtccagctgtgtcactgtcgtggtcgtgaggaagccgtggagctcaagtgaaggtgcc 120

QY 121 tgcagaagctccggtacacatctcactgtatctgtatatacaatgaggtctc 180
|||||
DB 121 tgcagaagctccggtacacatctcactgtatctgtatatacaatgaggtctc 180

QY 181 ggaacggcctcgtatgtatgttgatataattatctatgtatatacaatcaac 240
|||||
DB 181 ggaacggcctcgtatgtatgttgatataattatctatgtatatacaatcaac 240

QY 241 cagaagtttaaggcacaagcccaatgactgtagacaagctcagagcagcctatag 300
|||||
DB 241 cagaagtttaaggcacaagcccaatgactgtagacaagctcagagcagcctatag 300

QY 301 gaactagttctttagatctgaggaatacagccgttattactgtgcaagagcgcttg 360
|||||
DB 301 gaactagttctttagatctgaggaatacagccgttattactgtgcaagagcgcttg 360

QY 361 tatatgactactgtggtcgaaggtacccctgtcaccgtctcctca 405
|||||
DB 361 tatatgactactgtggtcgaaggtacccctgtcaccgtctcctca 405

RESULT 3
Q14802
Q14802 standard; DNA: 524 BP.

AC Q14802;
XX
DT 13-FEB-1992 (first entry)

XX Encodes murine anti-ICAM monoclonal antibody heavy chain.
DE
XX Intercellular adhesion molecule; variable region; V(H); mouse;
KW R6-5-D6 murine Mab; complementarily determining region; CDR; ds.
XX
OS Mus musculus.

XX
FH Key Location/Qualifiers
FT sig_peptide 34..90
FT /*tag= a
FT /standard_name= leader
FT CDS 34..524
FT /*tag= b

XX
XX W09116927-A.
XX
XX 14-NOV-1991.
XX
XX 29-APR-1991; 91WO-US02942.
XX
XX 27-APR-1990; 90GB-0009549.
XX
XX (CELL-) CELLTRECH LTD.
XX (BOEH) BOEHRINGER INGELHEIM PHA.
XX
XX Adair JR, Athwal DS, Rothlein RA;
XX
XX WPI: 1991-353533/48.
XX
XX P-PSDB: R15060.
XX
XX New humanised CDR-grafted anti-ICAM antibodies - used to treat
XX and prevent inflammation (e.g. psoriasis) tumours, viral
XX infections and asthma and in diagnosis

XX
PS Disclosure; Fig 2; 83bp; English.
XX

CC The heavy chain sequence was isolated from a cDNA library prepd. from
CC hybridoma cell line R6-5-D6 which secretes murine IgG2a/Kappa
CC antibody. The library was screened using a 980bp BamHI-EcoRI
CC fragment of a previously isolated mouse IgG2a constant region
CC clone. The murine framework-encoding sequences (i.e. not encoding
CC CDRs) will be replaced by human framework sequences to produce
CC recombinant (CDR-grafted humanised) antibody molecules having
CC specificity for ICAM-1.
XX
SQ Sequence 524 BP; 128 A; 130 C; 135 G; 131 T; 0 other;

Query Match 68.4%; Score 277.2; DB 12; Length 524;
Best Local Similarity 81.4%; Pred. No. 5e-67;
Matches 337; Conservative 0; Mismatches 68; Indels 9; Gaps 1;

QY 1 atgggttggaactgtatcatcttcttcttggttacacagctacaggtgtgacatccag 60
|||||
DB 34 atgggttggaactgtatcatcttcttcttggttacacagctacaggtgtgacatccag 93

QY 61 gtccagctgtgtcactgtcgtggtcgtgaggaagccgtggagctcaagtgaaggtgcc 120
|||||
DB 94 gtccagctgtgtcactgtcgtggtcgtgaggaagccgtggagctcaagtgaaggtgcc 153

QY 121 tgcagaagctccggtacacatctcactgtatctgtatatacaatgaggtctc 180
|||||
DB 154 tgcagaagctccggtacacatctcactgtatctgtatatacaatgaggtctc 213

QY 181 ggaacggcctcgtatgtatgttgatataattatctatgtatatacaatcaac 240
|||||
DB 214 ggaacggcctcgtatgtatgttgatataattatctatgtatatacaatcaac 273

QY 241 cagaagtttaaggcacaagcccaatgactgtagacaagctcagagcagcctatag 300
|||||
DB 274 cagaagtttaaggcacaagcccaatgactgtagacaagctcagagcagcctatag 333

QY 301 gaactagttctttagatctgaggaatacagccgttattactgtgcaagagcgcttg 360
|||||
DB 334 gaactagttctttagatctgaggaatacagccgttattactgtgcaagagcgcttg 393

QY 361 -----tatatgactactgtggtcgaaggtacccctgtcaccgtctcctca 405
|||||
DB 394 ttactactcctcttgactactgtggtcgaaggtacccctgtcaccgtctcctca 447

RESULT 4
Q14652
Q14652 standard; CDNA: 524 BP.

AC Q14652;
XX
DT 14-FEB-1992 (first entry)

XX R6-5-D6 anti-ICAM-1 heavy chain.
DE
XX Intercellular adhesion molecule-1; antibody; chimaeric; ds.
KW
XX
XX Mus musculus.

XX
FH Key Location/Qualifiers
FT sig_peptide 34..90
FT /*tag= a
FT CDS 91..524
FT /*tag= b

XX
XX W09116928-A.
XX
XX 14-NOV-1991.
XX
XX 29-APR-1991; 91WO-US02946.

xx	27-Apr-1990;	90GB-0009548.	
PR			
xx			
PA	(CELL-) CELLTECH LTD.		
xx	(BOEH) BOEHRINGER INGELHEIM PHA.		
xx			
PI	Adair JR, Robinson MK, Bright SM, Rothlein RA;		
xx			
DR	WPI: 1991-353534/48.		
xx	P-PSDE: R15200.		
xx			
PT	New humanised chimeric anti-ICAM-1 antibodies - useful in		
PT	treating inflammation e.g. psoriasis and ulcerative colitis to		
PT	suppress metastasis of haematopoietic tumour cell and in		
PT	diagnosis.		
xx			
PS	Claim 10; Fig 2; 85pp; English.		
xx			
CC	The sequence comprises the 5' untranslated region, signal sequence,		
CC	variable region and part of the constant region for the R6-5-6D		
CC	murine Mab heavy chain. The hybridoma cell line R6-5-D6 producing		
CC	the anti ICAM-1 Ab was provided by Boehringer Ingelheim		
CC	Pharmaceuticals Inc. The cells were grown and mRNA isolated and		
CC	used to prepare cDNA for a library in pSP64 vector DNA. The		
CC	library was grown in E. coli LM1035 and colonies screened using a		
CC	probe complementary to a sequence in the mouse kappa constant		
CC	region or with a 980 bp BamHI-EcoRI restriction fragment of a		
CC	previously isolated mouse IgG2a constant region clone. Ten		
CC	positive clones were isolated and rescreened. Positive clones from		
CC	the second round of screening were grown and the DNA inserts		
CC	sequenced. The DNA was used to construct a humanised Abs having		
CC	chimeric variable regions, esp. with IgG human constant region		
CC	domains. The Abs can be used to treat inflammation, to suppress		
CC	metastasis of haematopoietic tumour cells and growth of ICAM-1		
CC	expressing tumour cells, to treat viral infection, to suppress		
CC	extravascular migration of virally infected leucocytes and to treat		
CC	asthma.		
CC	See also Q14651 and Q14830.		
xx			
SQ	Sequence 524 BP; 128 A; 130 C; 135 G; 131 T; 0 other;		
	Query Match	68.4%; Score 277.2; DB 12; Length 524;	
	Best Local Similarity	81.4%; Pred No. 5e-67;	
	Matches 337; Conservative 0; Mismatches 66; Indels 9; Gaps		
OY	1 atgggtctgaactgtatcatctctcttcgtgtaccacagctcaggtgtgactccag	60	
DB	34 atgggttgagctgtatcatctctcttcgtgtaccacagctcaggtgtgactccag	93	
OY	61 gtccagctggtgcaagctctgggctcgaagtgaaagacctggagctcagtgaaagtgtcc	120	
DB	94 gtccagctgcaagctctgggctcgaagtgaaagacctggagctcagtgaaagtgtcc	153	
OY	121 tgcgaagcttcggcgtaaccatctcgtgtatgtcatatcagttgggtggaagctctc	180	
DB	154 tgcgaagcttcggcgtaaccatctcgtgtatgtcatatcagttgggtggaagctcat	213	
OY	181 ggcacgggctcgaagtgaattgagctataatattactatgataaataaacatacaac	240	
DB	214 gcaaaagagctcgaagtgaattgagctataatattactatcctcgtgacacaatacaac	273	
OY	241 csgaagtttaaggcgaagccacaatgactgtagacaagtcgacgacagcctataty	300	
DB	274 csgaagtttaaggcgaagccacaatgactgtagacaagtcgacgacagcctataty	333	
OY	301 gaactagttctttgagatctgagatacgaagccgtttatctactgtgcaagcgctctg	360	
DB	334 gaactgtcagaatgacactctgagatctgcacatcatattactgtgcaagagggatyg	393	
OY	361 -----tataatgactcgtgggtgaagttacacctgtgacgtctcccca	405	
DB	394 ttactactctcttgactactcgtgggtgaagttacacctcttcaagttctcccca	447	

RESULT	5	
ID	005554	
XX	Q05554 standard; DNA: 446 BP.	
AC	Q05554:	
XX		
DT	10-DEC-1990 (first entry)	
XX		
DE	Sequence encoding variable region of murine AHT 107 heavy chain.	
XX		
KM	Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; SS;	
XX		
OS	Mus sp.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	45..446
FT		/*tag= a
XX		
PN	EP380068-A.	
XX		
PD	01-AUG-1990.	
XX		
PF	24-JAN-1990; 90EP-0101351.	
XX		
PR	04-DEC-1989; 89US-0441702.	
XX		
PR	24-JAN-1989; 89US-0301216.	
XX		
PA	(MOLE-) MOLECULAR THERAPEU.	
XX		
PI	zerler B;	
XX		
DR	WPI: 1990-232892/31.	
XX		
DR	P-PSDB: R06250.	
XX		
PT	Expression vectors for producing chimeric monoclonal antibodies -	
XX		
PT	which express human constant region and non-human variable region	
XX		
PS	Disclosure: ; P; English.	
XX		
CC	MAbs comprising mouse CH and CL constant regions with human	
XX		
CC	variable regions may be used to create mouse/human hybrid MAbs,	
XX		
CC	which have a longer serum half-life. Method can be used to produce	
XX		
CC	Abs against interleukin-2 receptor and tumour necrosis factor.	
XX		
SQ	Sequence 446 BP; 117 A; 110 C; 113 G; 106 T; 0 other;	
Query Match		
Best Local Similarity 67.2%; Score 272.2; DB 11; Length 446;		
Matches 329; Conservative 81.2%; Pred. No. 1,1e-65;		
Mismatches 73; Indels 3; Gaps 1;		
QY	1 atgagctggaactctatcatctctctctctggttaccacagctacagtggtgactccag 60	
DB	45 atggctgtgagactgtatcatctctctctctctgagcagcagctacagtggtgactccag 104	
QY	61 gtccagctgtgcatctctggtggtctgaagtgaaagagcctggagagctcaagtgaagtgtrcc 120	
DB	105 gtccagctgtgcatctctggtggtctgaagtgaaagcctggagagctcaagtgaagtgtrcc 164	
QY	121 tgcacagctccggtctacacatctcaactgattatgctatatacagtggtgagacagctcct 180	
DB	165 tgcagaggtctcggtctacacatctcaactgattatgctctgcaetggtggaagagagtcatt 224	
QY	181 ggacagggcctcgtgagtgagtgagttatataattactatgatatacaacaactacaac 240	
DB	225 gcaagagctctagagtgagttggaattatagttcttaccatggtgatatacaagctacac 284	
QY	241 cagaagtttaaaaggcaagggcacaatgactgtgaagcaagtcgacgagacagcctatag 300	
DB	285 ccgaagtttaaaaggcaagggcacaatgactgtgaagcaatctctcagacagcctatag 344	

01	301	gaacttgcttcttgagatcgcgaagacgcgccttatctacgtgcgaagagcgctcg	36
02	302		41
03	303	gaattccagatgatgacatcgcgaagattcgcgcattcatctatcacgtgcgaaga	86
04	304	-----ggaagc	91
05	305		96
06	306		101
07	307		106
08	308		111
09	309		116
10	310		121
11	311		126
12	312		131
13	313		136
14	314		141
15	315		146
16	316		151
17	317		156
18	318		161
19	319		166
20	320		171
21	321		176
22	322		181
23	323		186
24	324		191
25	325		196
26	326		201
27	327		206
28	328		211
29	329		216
30	330		221
31	331		226
32	332		231
33	333		236
34	334		241
35	335		246
36	336		251
37	337		256
38	338		261
39	339		266
40	340		271
41	341		276
42	342		281
43	343		286
44	344		291
45	345		296
46	346		301
47	347		306
48	348		311
49	349		316
50	350		321
51	351		326
52	352		331
53	353		336
54	354		341
55	355		346
56	356		351
57	357		356
58	358		361
59	359		366
60	360		371
61	361		376
62	362		381
63	363		386
64	364		391
65	365		396
66	366		401
67	367		406
68	368		411
69	369		416
70	370		421
71	371		426
72	372		431
73	373		436
74	374		441
75	375		446
76	376		451
77	377		456
78	378		461
79	379		466
80	380		471
81	381		476
82	382		481
83	383		486
84	384		491
85	385		496
86	386		501
87	387		506
88	388		511
89	389		516
90	390		521
91	391		526
92	392		531
93	393		536
94	394		541
95	395		546
96	396		551
97	397		556
98	398		561
99	399		566
100	400		571
101	401		576
102	402		581
103	403		586
104	404		591
105	405		596
106	406		601
107	407		606
108	408		611
109	409		616
110	410		621
111	411		626
112	412		631

Query Match Similarity	65.6%	Score 265.8	DB 19	Length 1767
Best Local Similarity	78.5%	Pred. No. 9.3e-64		
Matches 318	Conservative	0	Mismatches 87	Indels 0
				Gaps 0
QY	1	atgggtctggaactgtgatactctctcttcctgtgttaccacagactacagatgctgcacctccag	60	
Db	1	atggatgtgagctgtgatactctctctctctctctctccgttcacgagactgcagcgctccactctg	60	
QY	61	gtccgcgcctggtgtcgaatctctggggctctgaagtgaaagacccgtggagctcaatgtgaagtgctcc	120	
Db	61	gtgcgcgcctgtgcgaatctctggggctctgaagtgaaagacccgtggagctcaatgtgaagtgctcc	120	
QY	121	tgcgaagcttcgcggctacacatctcaactctgtattgtgcatacagtggtgtgagacaggtctcc	180	
Db	121	tgcgaagctcttcgcgataccctctcaactcgtacataataatgcatgtggctgtgccagggccccc	180	
QY	181	ggacagagcgcctcgaatgtgaattgagatttaataattactatgaataatacaaatcaaac	240	
Db	181	ggacagaagactcgaatgtgattgagatatattatctcttaacaatgtgtgtactgctgcataac	240	
QY	241	cagaagatttaagggcaaaagcccaaatgaactgtagaacaagtctgacggagcacaagctatay	300	
Db	241	cagaagattcaaaagacaagggccacatgtgactgttgaaacatctcggcgagcacaagctcaay	300	
QY	301	gaactatgctctcttgagatctgagatctgagatacagcgcgttattactgtgcagaagcggtcctg	360	
Db	301	gagctgtgagcgcctgcatctgagatctgaagacaacgcgtctgtgtattactgtgcggaagtactat	360	
QY	361	tatatagactactgtgggtcgaagatataacctctgtccacgcttctctca	405	
Db	361	gctataggactactgtgggtccagagaaacctcgtgttcaacgcttctctca	405	

XX	DE	Anti-human Fas immunoglobulin M heavy chain DNA sequence SEQ ID #85.
XX	DE	Anti-rheumatic agent; immunoglobulin M; IgM; apoptosis inducer;
XX	KW	immunosuppression; autoimmune disease; treatment; rheumatism;
XX	KW	anti-Fas antibody; ss.
XX	OS	Synthetic.
XX	PN	JP2000154149-A.
XX	PD	06-JUN-2000.
XX	PF	17-SEP-1999; 99JP-0263984.
XX	PR	18-SEP-1998; 98JP-0264598.
XX	PA	(SANY) SANKYO CO LTD.
XX	DR	WPI: 2000-454476/40.
XX	DR	P-PSDB, B12917.
XX	PT	Anti-human Fas humanizing antibody-containing antirheumatic agents -
XX	PS	Example 2; Page 73-75; 109pp; Japanese.
XX	CC	The present invention relates to antirheumatic agents which comprise as
XX	CC	active ingredients an immunoglobulin M (IgM) protein. The IgM protein
XX	CC	does not include a J segment, has apoptosis inducing activity, and
XX	CC	consists of a light and heavy chain polypeptide produced synthetically.
XX	CC	The agents of the invention exhibit antirheumatic and immunosuppressive
XX	CC	activity and can be used to treat autoimmune diseases, especially
XX	CC	rheumatism. The IgM molecule used in the invention has human Fas-antigen

CC binding properties. Included in the invention are nucleotide sequences of
CC the IgM light and heavy chains (see A78267-A78272) and the corresponding
CC protein sequences (see B12913-B12918 and B12919), and nucleotide
CC sequences of the humanised anti-human Fas Ig chain1 (see A78202-A78206) and
CC protein sequences (see B12908-B12910). Also included are anti-human Fas
CC antibody CDR peptides (B12902-B12907). Primers specific for the
CC anti-human Fas antibody, light, heavy and kappa chains used in the
CC invention are represented by sequences A78213-A78266. Primers used for
CC sequencing the human Ig DNA used in the invention are represented by
CC sequences A78277-A78318 and A78335-A78337, while humanised anti-Fas Ig
CC DNA sequencing primers are represented by sequences A78321-A78334 and
CC A78338-A78357. Primer sequences A78207-A78212 are specific for murine Ig
CC DNA, and are used in the production of the agent of the invention.

Query Match	65.6%	Score 265.8	DB 21	Length 1767
Best Local Similarity	78.5%	Pred. No. 9.3e-64		
Matches 318	Conservative 0	Mismatches 87	Indels 0	Gaps 0

[illegible]

RESULT	8	
ID	V61364	
	V61364 standard; cDNA to mRNA, 1768 bp.	
XX		
AC	V61364;	
DT	18-JAN-1999 (first entry)	
DE	Anti-human Fas humanised antibody CH11 heavy chain Hmum cDNA.	
XX		
KM	Humanised antibody; Fas; CH11: monoclonal antibody; Mab; apoptosis	
KW	autoimmune disease; rheumatoid arthritis; therapy; human;	
KX	antibody engineering; ds.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..1767
FT		/*tag- a
FT	sig-peptide	1..57
FT*		/*tag- b
FT	mat-peptide	58..1764

FT		/+tag- C
XX		
PN	EP866131-A2.	
XX		
PD	23-SEP-1998.	
XX		
PF	20-MAR-1998;	98EP-0302113.
XX		
PR	21-MAR-1997;	97JP-0067938.
XX		
PA	(SANY) SANKYO CO LTD.	
XX		
PI	Haruyama H, Nakahara K, Serizawa N, Takahashi T;	
PI	Yonehara S;	
XX		
DR	WPI: 1998-482965/42.	
DR	P-PsDB: W71881.	
XX		
PT	Production of anti-Fas protein humanised antibodies - for use in	
PT	inducing apoptosis on Fas expressing cells in the treatment of	
PT	autoimmune diseases, especially rheumatoid arthritis	

PS Example 3; Page 108-110; 187pp; English.

CC This cDNA sequence codes for a humanised anti-Fas antibody CH11
CC heavy chain (see W71881), designated HnmM. HnmM is based on the
CC light chain (see W71888) of murine anti-human Fas monoclonal
CC antibody CH11. The humanised sequence was designed onto acceptor
CC selection of donor residues from CH11 to be grafted onto acceptor
CC molecule 21.28/CL. 2 light chain sequences (see W71880-81) have
CC been designed, and each can be used in combination with any of 4
CC light chain sequences (see W71876-79) to provide novel, claimed
CC humanised CH11 IgM1 antibodies that lack a J chain. These humanised
CC anti-human Fas antibodies are capable of inducing apoptosis in cells
CC expressing Fas (e.g. synovialocytes) and are useful in the treatment
CC of autoimmune disease and chronic rheumatoid arthritis. DNA
CC sequences encoding the humanised antibodies are claimed, as are
CC vectors such as phumM-1 including the HnmM nucleotide sequence,
CC and host cells such as *Escherichia coli* phumM-1 (FERM BP-5864).

Query Match	65.6%	Score 265.8	DB 19	Length 1768
Best Local Similarity	78.5%	Pred. No. 9.3e+64		
Matches 318	Conservative	0	Mismatches 87	Indels 0
				Gaps 0

[illegible]

Db .361 gctatgactactggggccagggaacctgctacacctctccta 405

RESULT 9

ID A78272 standard; DNA: 1768 BP.

XX AC A78272;

DT 16-NOV-2000 (first entry)

DE Anti-human Fas immunoglobulin M heavy chain DNA sequence SEQ ID #87.

KW Antirheumatic agent; immunoglobulin M; Igm: apoptosis inducer;

KW immunosuppression; autoimmune disease; treatment; rheumatism;

KM anti-Fas antibody; ss.

OS Synthetic.

PN JP2000154149-A.

PD 06-JUN-2000.

PF 17-SEP-1999; 99JP-0263984.

PR 18-SEP-1998; 98JP-0264598.

PA (SANY) SANKYO CO LTD.

DR WPI: 2000-454476/40.

DR P-PSDB; B12918.

PT Anti-human Fas humanizing antibody-containing antirheumatic agents

PS Example 2; Page 77-79; 109pp; Japanese.

XX The present invention relates to antirheumatic agents which comprise as
CC active ingredients an immunoglobulin M (IgM) protein. The IgM protein
CC does not include a J segment, has apoptosis inducing activity, and
CC consists of a light and heavy chain polypeptide produced synthetically.
CC The agents of the invention exhibit antirheumatic and immunosuppressive
CC activity and can be used to treat autoimmune diseases, especially
CC rheumatism. The IgM molecule used in the invention has human Fas-antigen
CC binding properties. Included in the invention are nucleotide sequences of
CC the IgM light and heavy chains (see A78267-A78272) and the corresponding
CC protein sequences (see B12913-B12918 and B12919), and nucleotide
CC sequences of the humanised anti-human Fas Ig CH11 (see A78202-A78206) and
CC antibody CDR peptides (B12902-B12907). Also included are anti-human Fas
CC anti-human Fas antibody, light, heavy and kappa chains used in the
CC invention are represented by sequences A78213-A78266. Primers used for
CC sequencing the human Ig DNA used in the invention are represented by
CC sequences A78277-A78318 and A78335-A78337, while humanised anti-Fas Ig
CC DNA sequencing primers are represented by sequences A78321-A78334 and
CC A78338-A78367. Primer sequences A78207-A78212 are specific for murine Ig
CC DNA, and are used in the production of the agent of the invention.
XX

Sequence 1768 BP: 387 A; 564 C; 485 G; 332 T; 0 other;

Query Match 65.6%; Score 265.8; DB 21; Length 1768;

Best Local Similarity 78.5%; Pred. No. 9.3e-64;

Matches 318; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 1 atgggttggaactatcatctctctctggtaccacagctacaggtgtgactccag 60
DB 1 atggagtatgagctgagctctctctctctccctgcagacagcagcgctccactctg 60
QY 61 gfcacagcgtgtgcaactctgtggagctgagtggaagaagcctggagctcagatgagtgctcc 120
DB 61 gtgcagctgtgtgcaactctgtggagctgagtggaagaagcctggagcctcagatgagtgctcc 120
QY 121 tgcagaactctgcggtacacatcactgtatgtatatacagtggtgagacagtgctct 180

DB 121 tgcagaactctgcggtacacatcactgtatgtatatacagtggtgagacagtgctct 180
QY 181 ggcacagggcctcgcagctgagctgtgagttattattactatgataatacaactacaac 240
DB 181 ggaagaagcctcgcagctgagctgtgagttattattactatgataatacaactacaac 240
QY 241 cagaagtttaaggcagaagccacatgactgtagacaagctgacagacagcctatag 300
DB 241 cagaagtttaaggcagaagccacatgactgtagacaagctgacagacagcctatag 300
QY 301 gaactagctcttgagactcagagtaagcgcgtttattactgtgcgaagcggcctg 360
DB 301 ggcctgagcagcctgagactcagagtaagcgcgtttattactgtgcgaagcggcctg 360
QY 361 tatatgactactgggtgcaagtaacctgttcacgcgtctccta 405
DB 361 gctatgactactggggccagggaacctgctacacctctccta 405

RESULT 10

ID T42717 standard; DNA: 424 BP.

XX AC T42717;

DT 04-FEB-1997 (first entry)

DE HuM3 VH coding sequence.

KW Humanised antibody; variable heavy region; buried residue modification;

KW VH; HuM3 VH; BA46 antigen; human; milk fat globule; HMFG; lactation;

KW fat globule membrane; murine; mammary; epithelial cell; breast cancer;

KW breast membrane glycoprotein; therapy; immunotherapy; ss.

OS Synthetic.

FT Key Location/Qualifiers

FT CDS 11..418

FT /tag= a

FT /product= HuM3 VH (BR-M version)

PD WO9608565-A2.

PF 21-MAR-1996.

PF 14-SEP-1995; 95WO-0511683.

PR 07-JUN-1995; 95US-0487598.

PR 16-SEP-1994; 94US-0307868.

PA (CANC-) CANCER RES FUND CONTRA COSTA.

DR Certiani RI, Do Couto FJR, Peterson JA;

DR WPI: 1996-179941/18.

DR P-PSDB; W06442.

PT Recombinant MC3 antibody which binds BA46 antigen of HMFG -

PT comprises a modified heavy or light chain variable region, useful in

PT the diagnosis and therapy of breast cancer

PS Claim 13; Fig 18; 91pp; English.

XX This sequence represents the coding sequence for the variable heavy (VH)

XX chain of the humanised murine antibody HuM3 VH. The MC3 VH sequence was

XX humanised using the buried residue modification technique, where

XX important non-human framework residues are unaffected. The MC3 antibody

XX binds to the BA46 antigen of the human milk fat globule (HMFG). The milk

XX fat globule membrane is derived from the apical surface of the mammalian

XX epithelial cell during lactation, and therefore is a source for breast

XX membrane glycoproteins. The antibody can be used in an in vitro method

XX to detect a HMFG antigen (or antigen fragment), and to diagnose the

	CC	pCR amplification (see V70115-17), and includes humanising R46G
	CC	and A/T87 amino acid substitutions. Host cell Escherichia coli
	CC	pGHADH93 SANK 7029d harbors plasmid pGHDPHV3 carrying a fusion
	CC	fragment of the humanised HV type HFE7A heavy chain and DNA
	CC	encoding human IgM constant region, and is deposited as
	CC	FERM-BF-6273 (claimed). The invention provides methods for
	CC	producing humanised antibodies by culturing host cells. Humanised
	CC	versions of HFE7A (see W83031-37), like native HFE7A, are capable
	CC	of inducing apoptosis in abnormal cells expressing Fas, and of
	CC	inhibiting Fas-induced apoptosis in normal cells. The humanised
	CC	antibodies are used to evaluate, in animal models, treatments of
	CC	diseases that involve Fas/Fas ligand interactions, and also to
	CC	treat such diseases, including autoimmune disease (e.g., systemic
	CC	lupus erythematosus, Hashimoto's disease, graft versus host disease,
	CC	Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,
	CC	Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,
	CC	autoimmune haemolytic anaemia, sterility, myasthenia gravis,
	CC	multiple scleros, Basedow's disease, thrombopenia purpura and
	CC	insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
	CC	mycocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
	CC	anaemia, hepatitis, AIDS and transplant rejection (all claimed).
	XX	
	SEQ	Sequence 2071 BP; 460 A; 685 C; 561 G; 365 T; 0 other;
	Query Match	62.6%; Score 253.6; DB 19; Length 2071;
	Best Local Similarity	77.6%; Pred. No. 2..2e-60;
	Matches 326; Conservative	0; Mismatches 79; Indels 15; Gaps
OY	1	atgggttggaactgatatcatcttcttccttgtaccacagcgcagtgtgccctccag 60
DQ	21	atgggatgaggcgtagtatcacctctctctgtgtacacacgcatacaagglytcccactccaag 80
OY	61	gtccgcagctgtcagatcctgggctgtgaagtcgaagaagccggggagccagtcgaagtgctcc 120
DQ	81	gtccccaaacygtgcagctctggggctgtgaagtcgaagaagccggggagccagtcgaagtgctcc 140
OY	121	tgcnaaacctccggtcacacattcatactgatatcatalacagttgggtlgagacaagtgctcc 180
DQ	141	tgcnaagctcttcgtacctacacattccacagctaactgtagtcagcgggttaaaaacagccctc 200
OY	181	ggacacagggcctcgcagatggaattgagattaatattaattactatgatatatacaaactacaac 240
DQ	201	ggacacagggcctctgagatggaattgagattatgacctcttgatagcataactaactaactaal 260
OY	241	cgaagatttaaaggcgaaggccaactgactgttgaaaaagtcgacggcgacagagcctaatg 300
DQ	261	caaaagttcaaggcgaaggccaactgactgttgaaaacatccactgcaagcctacatg 320
OY	301	gaactagatctcttggagatcgaagatcacggccgttatatactatgtaacaaga----- 351
DQ	321	ggagctcagcagcctgagatcgtagsgacaagcgcgcttatatactatgtaagaabaataggac 380
OY	352	- - - gggcctbgatataagactactcgggtgcacaagtiacccctgttacccgctctoctca 405
DQ	381	tatagtaaacactgfatcttgatgcagtctggggggaaggacccctgttcacccgctctoctca 440
RESULT	13	
AZ1B4	A72184	A72184 standard; DNA; 2071 BP.
AC	A72184:	
DT	24-NOV-2000	(first entry)
DE		DNA encoding humanised anti-Fas antibody heavy chain, SEQ ID NO:116.
KW		Anti-Fas antibody: monoclonal antibody HFE7A; FERM-BP-5828;
KX		murine; humanised antibody; complementarity determining region; CDR;
KM		human Fas; Fas ligand; apoptosis modulator; programmed cell death;
KJ		autocrine disease; allergy; atopy; arteriosclerosis; myocarditis;
KN		cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;

KM	hepatitis;AIDS; graft rejection, heavy chain; ds.
XX	
OS	Chimeric - Mus musculus.
XX	Chimeric - Homo sapiens.
PN	JP2000169393-A.
PD	20-JUN-2000.
PF	30-SEP-1999; 99JP-0278301.
PR	30-SEP-1998; 98JP-0276883.
PA	(SANY) SANKYO CO LTD.
DR	WPI: 2000-485645/43.
DR	P-PSDB: B14779.
PT	Preventive or treating agent for the diseases caused by an abnormality
PT	in the Fas/Fas ligand system e.g. autoimmune diseases, contains
PS	anti-Fas antibody
XX	
PS	Example 22; Page 106-108; 139pp; Japanese.
XX	
CC	The invention relates to compositions for the prevention or treatment
CC	of diseases caused by an abnormality in the Fas/Fas ligand system
CC	containing an anti-Fas antibody as the active component. The anti-Fas
CC	antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
CC	or a humanised version of HFE7A containing identical CDRs
CC	(complementarity determining regions) to antibody HFE7A. Via its
CC	interaction with Fas, the antibody of the invention acts as a modulator
CC	of apoptosis. The compositions of the invention may therefore be used in
CC	the treatment or prevention of conditions such as autoimmune diseases,
CC	allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
CC	glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
CC	and organ graft rejection. Sequences A72146, A72159 and A72184
CC	represent DNA encoding the heavy chains (or fragments thereof) of
CC	various humanised HFE7A-derived anti-Fas antibodies.
XX	
SQ	Sequence 2071 BP; 460 A; 685 C; 561 G; 365 T; 0 other;
Query Match	62.6%; Score 253.6; DB 21; Length 2071;
Best Local Similarity	77.6%; Pred. No. 2.2e-60;
Matches 326; Conservative	0; Mismatches 79; Indels 15; Gaps
1;	
QY	1 atgggtctggaactcgtatcatccttcttccttggtttacacaagctcacagtggtgcacctccag 60
DG	
DG	21 atggatgatgagctgatacatcctctctcttcttggttagacaacagctaacagtggtccacctcg 80
QY	61 gtccaagctcggtgcagttctcggggcttgaggttgaagaagctctggagctcaagtgaagtgctc 120
DG	
DG	81 gtccaacatcggtgcagttctcggggcttgaggttgaagaagctctggggcttcagtggaagtgctc 140
QY	121 tgcagaagcttcgggttacacattcacttgatatagtatacaaaatgggtgtagaagaagctctc 180
DG	
DG	141 tgcagaagcttcgggttacacattcacttcaccgcagctactgtagcagtggtgtaaaacaggctcc 200
QY	181 ggaacaggctctcgagtgagttgagttatlaatatlaattactaatgatalaatacaactacaac 240
DG	
DG	201 ggaacaggctctcgagtgagttgagttgagttgagttgagttgagttgagttgagttgagttgag 260
QY	241 cagaagtttaaggggaagaagccacaatlgactgtagaagaagtgtagaagaagcagcttatatg 300
DG	
DG	261 caaagtttaaggggaagaagccacaatlgactgtagaagaagtcacatcaactagaacagctcatag 320
QY	301 gaacttattctcttgagatctcgagatatacggccgtttaattactgtgcaaga----- 351
DG	
DG	321 gagctcagcagccttgagttctgaggaacagccgctgctatacttactgtgcaagaataaggac 380
QY	352 -----ggcgccctggtatatagtgaactactcgggggtgcaagtgatacccttgtcaacgtctctcca 405
DG	
DG	361 tatagtaaacaactctgtaacttcgattctcgttcggggcggaaggaagcacttgtaacagctctcccta 440

RESULT	14	
ID	A11622	
XX	A11622 standard: DNA: 2071 BP.	
XX		
XX	A11622:	
XX		
DT	08-AUG-2000 (first entry)	
XX		
DE	Humanised HFE7A designed heavy chain DNA #2.	
KW	Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;	
KW	anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant;	
KW	dermatologic; immunosuppressive; thymometric; antirheumatic; anti-Fas;	
KW	neurotropic; antifertility; neuroprotective; antiarteriosclerotic;	
KW	hepatotropic; humanized; apoptosis; systemic lupus erythematosus;	
KW	Hashimoto disease; rheumatoid arthritis; graft versus host disease;	
KW	Strogen's syndrome; anemia; Addison's disease; scleroderma; sterility;	
KW	Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;	
KW	multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;	
KW	insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;	
KW	cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; ss.	
XX		
OS	Synthetic.	
XX		
PN	EP90663-A2.	
PD		
PD	05-APR-2000.	
XX		
PF	29-SEP-1999; 99EP-0307711.	
XX		
PR	30-SEP-1998; 98JP-0276881.	
PR	30-SEP-1998; 98JP-0276882.	
XX		
PA	(SANKYO) SANKYO CO LTD.	
XX		
PI	Serizawa N, Hanyama H, Nakahara K, Tamaki I, Takahashi T;	
DR	WPI: 2000-258930/23.	
DR	P-PSDB; W90929.	
XX		
PT	New humanized anti-Fas antibody, useful for treating or preventing e.g.	
PT	inflammatory or autoimmune disease, induces apoptosis selectively in	
PT	cells with abnormal Fas-Fas ligand systems	
XX		
PS	Example reference 22; Page 148-150; 263pp; English.	
XX		
XX	This invention describes a novel humanized anti-Fas antibody-like	
CC	molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas	
CC	ligand system, by binding to Fas on the cell surface, and prevents	
CC	apoptosis in cells with a normal system, by inhibiting binding between	
CC	Fas and its ligand. The products of the invention have anti-inflammatory,	
CC	anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,	
CC	immunomodulatory, dermatologic, immunosuppressive, thymometric,	
CC	antirheumatic, nephrotropic, antifertility, neuroprotective,	
CC	antiarteriosclerotic, cardiant and hepatropic activity. (I) induce	
CC	apoptosis by binding to cell surface Fas or inhibit it by competitive	
CC	inhibition of ligand binding. (I) are used to treat and/or prevent	
CC	diseases associated with the Fas/Fas ligand system, especially systemic	
CC	lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft	
CC	versus host disease, Strogen's syndrome, pernicious or hypoplastic	
CC	anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's	
CC	disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,	
CC	multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin	
CC	dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,	
CC	cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral	
CC	(B, C or D) or alcoholic), and transplant rejection. (I) selectively	
CC	inhibit apoptosis in normal cells but selectively induce it in abnormal	
CC	cells. They bind to both human and murine Fas, so can be evaluated in	
CC	murine disease models. (I) act on the active site of Fas, i.e. they mimic	
CC	the native ligand, do not induce liver disease, and have reduced risk of	
CC	inducing a human anti-murine antibody response. This sequence encodes	

Mon Apr 30 07:08:15 2001

us-09-249-011-5.rng

Page 12

Db 383 tatagtacaactggtactctgctgtctgtggccaagblacaactlgtlcaaccgtctctctca 442

Search completed: April 29, 2001, 20:39:39
Job time: 3486 sec

A; Title: Simultaneous expression of immunoglobulin mu and delta heavy chains by a clon

C:Idref: 02-Apr1982 #sequence.revision 02-Apr-1982.<text_change 22-Jun-1999
A:Accession: A90809; #B90809; A22769; A02034; A02035
R:Bothwell, A.L.M.; Paskind, M.; Rehn, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D.
Cell 24, 625-637, 1981
A:Title: Heavy chain variable region contribution to the NP(b) family of antibodies: some
A:Accession: A90809
A:Reference number: A90809; MUID:81234548
A:Molecule type: DNA
A:Residues: 1-139 <B18>
A:CROSS-references: GB:J00529; NID:g195114; PIDN:AAA38170.1; PID:g195115
A:Accession: B90809
A:Molecule type: DNA
A:Residues: 1-117 <I862>
A:Note: the B1-8 mu chain mRNA was cloned from a hybridoma making antibodies to the hapten
A:Note: the 186-2 germ-line gene was cloned from a library of C57BL/6 DNA
R:ildrop, R.; Bruggemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.
EMBO J. 1, 635-640, 1982
A:Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between
A:Reference number: A90971; MUID:84236026
A:Accession: A22769
A:Molecule type: protein
A:Residues: 20-139 <DIL>
A:Note: the V region of the B1-8 delta chain, derived as a spontaneous class switch variant
of the mu chain
C:Genetics: 1
A:Introns: 16/1
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-139/Product: Ig kappa chain V region (B1-8) #status experimental <MAT>
E:34-117/Domain: immunoglobulin homology <IMM>
F:118-124/Region: D segment
F:125-139/Region: J segment (JH2)

```

Query March      69.6% Score 501; DB 1; Length 139;
Best Local Similarity 68.3%; Pred. No. 6e-37;
Matches 95; Conservative 16; Mismatches 24; Indels 4; Gaps 1;

OY    1  MGWNCIIFFLVTTATGVSQVOLVQSAGAEVKKPGSSVRVSKCA$SGYTFTDYAIDWRQAP 60
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     1  MGWSCIMFLFATATGVHSVOLOOPGAELVPKGCASVSLKSCASGYTFTSYMHMVKORP 60
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
OY    61  GGGLGWICIVINYYNNTNVYNOKFKGAKMTVDK$NSTYAMELISLRSDTAVVYCAR--- 117
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     61  GGGLGWIRIDPN$SGTYNEKFNSKATLTVDKPSTAYMOLSSLTSDESAVYCARYD 120
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
OY    118 -AAAMYDMYGCGTLTVSS 135
      :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     121 YGSSYFDYMGOGTLTVSS 139
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT       7
A27609
Ig heavy chain precursor V region (I29) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 30-Jun-1991 #text_Change 23-Jul-1999
C:Accession: A27609
R:Klein, D.; Nleupski, J.; Sirtlin, S.; Stavnezer, J.
J. Immunol. 140, 1676-1684, 1988
A>Title: I.29 lymphoma cells express a nonmutated V-H gene before and after H chain switch
A:Reference number: A27609; MUID:88154467
A:Accession: A27609
A:Molecule type: DNA
A:Residues: 1-139 <KLE>
A:Cross-references: EMBL:M19401; NID:g195441; PIDD:AAA38303.1; PID:g553992
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
E:20-139/Product: Ig heavy chain V region I29 #status predicted <VAR>
F:34-117/Domain: immunoglobulin homology <IM>
```

[illegible]

```

RESULT      8
JL0076
Ig heavy chain precursor V region (anti-phenylloxazolone, 18C10) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_rev1sion 31-Dec-1991 #text_change 23-Jul-1999
C:Accession: JL0076
R:Kaartinen, M.; Rocca-Serra, J.; Maekela, O.
Mol. Immunol. 25, 859-865, 1988
A:Title: Combinatorial association of V genes: one VH gene codes for three non-cross-
A:Reference number: JL0076; MUID:8906973
A:Accession: JL0076
A:Molecule type: mRNA
A:Residues: 1-141 <KRA>
A:Cross-references: GB:M27788; NID:g195851; PID:AAA38441.1; PID:g195852
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <Sig>
F:20-141/Product: Ig heavy chain #status predicted <Mat>
F:34-111/Domain: immunoglobulin homology <IMM>
F:50-54/Region: complementarity-determining 1
F:69-85/Region: complementarity-determining 2
F:123-135/Region: C
F:136-141/Region: C2 segment

```

```

Query Match          69.2%; Score 498; DB 2; Length 141;
Best Local Similarity 69.6%; Pred. No. 1.le-36;
Matches    94; Conservative   15; Mismatches    26; Indels      0; Gaps      0;

OY      1  MGNMNIIFLVTATGAVHSQVQLVQSAGAEVKRKPGSSVAVSCASGYTFETDVALIQWVRQP 60
        |||::|||::| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB       1  MWMSCIMFLAATAFGVSHSQVLQOPGAELNPKGSAYKLSCKASGYTFTSYMMHWKARP 60
        |||::|||::| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY      61  GGGLGWIGIVINLYONTNVNOKFKRATMTYDKSRSTAYMELSSLRSSEDTAVYYCARAAW 120
        ||::|||||::| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB       61  GGLGEIWIIGIDNSGGTYKNKKFSKATLLTDKPSPSTAYMOLSLTSDESAVYYCAREGP 120
        ||::|||||::| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY      121 YMDYWGGGTFLTVSS 135
        |||::|||::| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB       121 AGDYWGQGTTTLTVSS 135
        |||::|||::| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT# 9
Ig heavy chain V region - human (fragment)
C.Species: Homo sapiens (man)
C.Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
C.Accession: A32483
R.Latrick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck
Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989
A.Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells
A.Reference number: A32483; MUID:89273586
A.Accession: A32483
A.Status: preliminary

```

A:Molecule type: mRNA
A:Residues: 1-142 <LAR>
A:Cross-references: GB:26463
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:25-108/Domain: Immunoglobulin homology <IMM>

Query Match	68.7%	Score	494.5	DB 2	Length	142			
Best Local Similarity	71.5%	Pred. No.	2.3e-36						
Matches	98	Conservative	10	Mismatches	18	Indels	11	Gaps	1

OY	10	LVTTFVGHSDVOLVLOSAGAEVKRFGSSKVKSCSKASGTFFEDUALONWRQAPGGLEIGV	69
Dd	1	LLAVARGAHSOVLVOQSAGAEVKRKPGASKVKSCAKSGTFFNNYIMHWKRAQPGGLEMGSI	60
OY	70	INIYIDNNTYNOKREKGRKTMTVDKSTSTAYWELSLSESDPAUYUCCARAMY-----	121
Dd	61	INPQSNSTNYAKOKROGRTMTTRDTSTIVTWELSLSESDPAUYIICAREKLATITFIEGLVI	120
OY	122	--MDYWGGFTLVTVSS 135	
Dd	121	ITYGMIDYWGCGTLVTVSS 137	

RESULT 10
S14683
Ig mu chain precursor, membrane-bound (clone 201) - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
A:Accession: S14683; 508047
R:Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
Nucleic Acids Res. 18, 4278, 1990
A:Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain
A:Reference number: S14683; MUID:90332450
A:Accession: S14683
A:Molecule type: mRNA
A:Residues: 1-627 <FRT>
A:Cross-references: EMBL:X17115; NID:g33450; PIDN:CAA34971.1; PID:g33451
C:Superfamily: Immunoglobulin C region: immunoglobulin homology
C:Keywords: immunoglobulin; membrane protein
F:1-15/Domain: signal sequence #status predicted <STG>
F:16-627/Product: Ig mu chain #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match	68.7%	Score	494.5	DB	2	Length	627
Best Local Similarity	65.8%	Pred. No.	1e-35				
Matches	100	Conservative	10	Mismatches	25	Indels	17
						Gaps	2

QY	1	NGMNCILFFLLVTTATTAAGVNSQVQLVQSGAEYKKPSSSVKYSCKRSGYFTYDIALIOWROAP	60
	1		
	1		
	1		
	1		
Db	1	MDMTWRFLEFVVAATGAGVQSQVLVQSGAEYKKPSSSVKYSCKRSGGTFSSYALISWRQAP	60
	1		
	1		
	1		
	1		
QY	61	GQGLGEMTICIVINLYDNNYINQKFKRKATMTVDKSTATYAMELSSLRSBEDIAYYYCAR---	117
	1		
	1		
	1		
	1		
Db	61	GQGLGEMTICIVINLYDNNYINQKFKRKATMTVDKSTATYAMELSSLRSBEDIAYYYCAR---	117
	1		
	1		
	1		
	1		
QY	118	-----AAMY-----MDYWGGLTVTVSS	135
	1		
	1		
	1		
	1		
Db	121	LGPISSGWTYPNSDIYYYGMDYWGGLTVTVSS	152
	1		
	1		
	1		
	1		

RESULT 11
H32513
Ig heavy chain precursor V region (BXMI6) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C:Accession: H32513
R:Kotler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;
J. Clin. Invest. 82, 852-860, 1988
A:Title: Immunoglobulin kappa light chain variable region gene complex organization and
Reference number: A94689; MUID:883331394

A:Accession : H32513
A:Molecule type: DNA
A:Residues: 1-137 <ROF>
A:Cross-references: GB:J02031; NID:q196949; PIDN:AAA38848.1; PID:q196950C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
C:34-11/Domain: Immunoglobulin homology <IMM>

Query Match	68.3%	Score 492;	DB 2;	length 137;
Best Local Similarity	66.4%	Pred. No. 3.6e-36;		
Matches 91;	Conservative 22;	Mismatches 22;	Indels 2;	Gaps 1;

[illegible]

RESULT 12
PH1482
Ig heavy chain V region (clones 36-35[TC] and X7-TC) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: PH1482; PH1495
R:Ginsli, A.M.; Manser, T
J. Exp. Med. 177, 797-809, 1993
A:Title: Hypermutation is observed only in antibody H chain V region transgenes that
d for somatic mutation.
A:Reference number: PH1482; MUID:93171820
A:Accession: PH1482
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-140 <GI>
A:Experimental source: hybridoma cell
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterodimer; immunoglobulin
/34-117/Domain: immunoglobulin homology <IMM>

Query Match	67.8%	Score 488.5	DB 2	Length 140
Best Local Similarity	65.7%	Pred. No. 7.5e-36		
Matches 92	Conservative 18	Mismatches 25	Indels 5	Gaps 1

[illegible]

```

RESULT 13 |
G2MS43 | Ig heavy chain precursor V region (S43) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 22-Jun-1999
C:Accession: A02038
C:Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore

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Search completed: April 25, 2001, 09:39:40
Job time: 178 sec


```

RESULT 2
HV07_MOUSE ID HV07_MOUSE STANDARD: PRT: 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION B1-8/186-2 PRECURSOR.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RX Botwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
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CC -----
CC EMBL: J00529; AAA38170.1; -.
DR PIR; A02034; MMS18.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; 19; 1.
DR KMW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 54 FRAMEWORK 2.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FDC9F465 CRC64;

Query Match 69.68; Score 501; DB 1; Length 139;
Best Local Similarity 68.3%; Pred. No. 3.1e-43;
Matches 95; Conservative 16; Mismatches 24; Indels 4; Gaps 1;

QY 1 MGNACITFLVTTATGVSQVLOVSGAEVKKPGSSSVKYSCKASGYFTDAIOWVQAP 60
DB 1 MGNWCMILFLAATVGVSHVQVLODPGAEFLVKGASVSKLSCKASGYFTSLMHVWVQRP 60
QY 61 GGGLEWIGVINIYDNTNPNYOKFKGKATMTVDKSTAYVELSLRSEDPVAVYCAR-- 117
DB 61 GGGLEWIGRIDPNPNSGCTTYDHFPSKATLTIDKPSSTAYMQLSLTSEDSAVYICARYD 120
QY 118 -AANYMDYWGCGTLTVSS 135
DB 121 TGSSEYFDYWGCGTLTVSS 139

RESULT 3
HV11_MOUSE

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ID HV11_MOUSE STANDARD: PRT: 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION S43 PRECURSOR.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RX Botwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
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CC -----
CC EMBL: J00539; AAA38172.1; -.
DR PIR; A02038; GMS43.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; 19; 1.
DR KMW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 54 FRAMEWORK 2.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

Query Match 67.88; Score 488; DB 1; Length 137;
Best Local Similarity 67.2%; Pred. No. 6e-42;
Matches 92; Conservative 15; Mismatches 28; Indels 2; Gaps 1;

QY 1 MGNACITFLVTTATGVSQVLOVSGAEVKKPGSSSVKYSCKASGYFTDAIOWVQAP 60
DB 1 MGNWCMILFLAATVGVSHVQVLODPGAEFLVKGASVSKLSCKASGYFTSLMHVWVQRP 60
QY 61 GGGLEWIGVINIYDNTNPNYOKFKGKATMTVDKSTAYVELSLRSEDPVAVYCAR--RA 118
DB 61 GGGLEWIGRIDPNPNSGCTTYDHFPSKATLTIDKPSSTAYMQLSLTSEDSAVYICARYL 120
QY 119 AWYMDYWGCGTLTVSS 135
DB 121 GRYDYWGCGTLTVSS 137

RESULT 4
HV48_MOUSE ID HV48_MOUSE STANDARD: PRT: 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

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DE IG HEAVY CHAIN V REGION TEPC 1017 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; Pubmed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RT Tucker P.W.;
RL "Illegitimate recombination generates a class switch from C mu to C
delta in an Igd-secreting plasmacytoma.";
DR Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR: A02033; HVMST7.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; signal.
FT CHAIN 1 20
FT SIGNAL 1 20
FT CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.
FT DOMAIN 21 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 128 138 FRAMEWORK 4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 748157EAC6907BB8 CRC64;

Query Match 67.7%; Score 487.5; DB 1; Length 138;
Best Local Similarity 68.8%; Pred. No. 6.8e-42;
Matches 93; Conservative 16; Mismatches 24; Indels 3; Gaps 1;

QY 1 MGNWCIIFLVTATGVSQVLOVSGAEVKKPGSSVKASCASYTFTDAIOWVRAP 60
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
DB 1 MGNWCIIFLVTATGVSQVLOVSGAEVKKPGSSVKASCASYTFTDAIOWVRAP 60
QY 61 GGGLEWIGVINYDNTNPNOKFKGATPTVDKSTAVAMELSSLRSEDTAVYCARAAW 120
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
DB 61 GGGLEWIGVINYDNTNPNOKFKGATPTVDKSTAVAMELSSLRSEDTAVYCARAAW 120
QY 121 YMD---YWGCGTLTVSS 135
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
DB 121 YMD---YWGCGTLTVSS 135
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|

RESULT 5
HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
RT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DR IG HEAVY CHAIN V REGION 9367 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A/J;
RX MEDLINE=82152818; Pubmed=6801765;
RA Sims J., Rabbits T.H., Estess P., Slaughter C., Tucker P.W.,
RT Capra J.D.;
RL "Somatic mutation in genes for the variable portion of the
   immunoglobulin heavy chain.";
DR Science 216:309-311(1982).
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CX -----
DR EMBL: J00493; AAA38128.1; -.
DR PIR: A02028; HVMSC7.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma; signal.
FT CHAIN 1 19
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 9367.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 254ACBBE31DA5CE8 CRC64;

Query Match 67.2%; Score 483.5; DB 1; Length 140;
Best Local Similarity 65.7%; Pred. No. 1.7e-41;
Matches 92; Conservative 17; Mismatches 26; Indels 5; Gaps 1;

QY 1 MGNWCIIFLVTATGVSQVLOVSGAEVKKPGSSVKASCASYTFTDAIOWVRAP 60
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
DB 1 MGNWCIIFLVTATGVSQVLOVSGAEVKKPGSSVKASCASYTFTSYGINVWKR 60
QY 61 GGGLEWIGVINYDNTNPNOKFKGATPTVDKSTAVAMELSSLRSEDTAVYCARAAW 120
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
DB 61 GGGLEWIGVINYDNTNPNOKFKGATPTVDKSTAVAMELSSLRSEDTAVYCARAAW 120
QY 121 Y-----MDYWGCGTLTVSS 135
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
DB 121 YGGSYDFYWGCGTLTVSS 140

RESULT 6
HV06_MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
RT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DR IG HEAVY CHAIN V REGION 102 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=81234548; Pubmed=6788376;
RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RT Baltimore D.;
RL "Heavy chain variable region contribution to the NPb family of
   antibodies: somatic mutation evident in a gamma 2a variable region.";
DE Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
DR PIR: A02032; HVMSC2.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; signal.
FT CHAIN 1 19
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FCAC8 CRC64;

Query Match 65.3%; Score 470; DB 1; Length 117;

```

Best Local Similarity 76.7%; Pred. No. 3,1e-40;
Matches 89; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 1 MGNMCIIFLVATATGVSQVQLVQSGAEVKKPSSSVKVCSSKAGYFTDTAIDWVQAP 60
DB 1 MGNMCIIFLVATATGVSQVQLVQSGAEVKKPSSSVKVCSSKAGYFTDTAIDWVQAP 60
QY 61 GGGLEWIGVINIYDNTNNOKEFGKATMTVDKSTAYMELSLRSEDPAVYYCAR 116
DB 61 GGGLEWIGRIHPSDDTNYNOKFKGKATLTVDKSSSTAYMQLSLTSEDSAVYYCA 116

RESULT 7

HV03_MOUSE STANDARD; PRT; 117 AA.

AC P01749;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG HEAVY CHAIN V REGION 3 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).

CC -I- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC -----
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CC -----
DR EMBL; J00536; AAA38605.1; -
DR PIR; A02031; HVMS3.
DR InterPro; IPR003006; -
DR Pfam; PF00047; 1g; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 3.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13016 MW; 427C861C53975EDC CRC64;

Query Match 64.3%; Score 463; DB 1; Length 117;
Best Local Similarity 75.6%; Pred. No. 1,6e-39;
Matches 90; Conservative 12; Mismatches 13; Indels 4; Gaps 2;

QY 1 MGNMCIIFLVATATGVSQVQLVQSGAEVKKPSSSVKVCSSKAGYFTDTAIDWVQAP 60
DB 1 MGNMCIIFLVATATGVSQVQLVQSGAEVKKPSSSVKVCSSKAGYFTDTAIDWVQAP 60
QY 61 GGGLEWIGVINIYDNTNNOKEFGKATMTVDKSTAYMELSLRSEDPAVYYCAR 117
DB 61 GGGLEWIG--NIYPSDSETHYNOKFKDKATLTVDKSSSTAYMQLSLTSEDSAVYYCAR 117

RESULT 8
HV04_MOUSE STANDARD; PRT; 117 AA.

AC P01748;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG HEAVY CHAIN V REGION 23 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).

CC -I- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC -----
DR PIR; A02030; HVMS23.
DR InterPro; IPR003006; -
DR Pfam; PF00047; 1g; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match 62.1%; Score 447; DB 1; Length 117;
Best Local Similarity 71.8%; Pred. No. 6,2e-38;
Matches 84; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 1 MGNMCIIFLVATATGVSQVQLVQSGAEVKKPSSSVKVCSSKAGYFTDTAIDWVQAP 60
DB 1 MGNMCIIFLVAAANGVSHQVQLVQSGAEVKKPSSSVKVCSSKAGYFTDTAIDWVQAP 60
QY 61 GGGLEWIGVINIYDNTNNOKEFGKATMTVDKSTAYMELSLRSEDPAVYYCAR 117
DB 61 GGGLEWIGINIPGNGTNYNEKFSKVTLTVDKSSSTAYTQLSLTSEDSAVYYCAR 117

RESULT 9

HV1B_HUMAN STANDARD; PRT; 117 AA.

AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG HEAVY CHAIN V-1 REGION H63 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=83144028; PubMed=6298778;
RA Rechevali G., Ram D., Glazer L., Zakut R., Givol D.;
RT "Evolutionary aspects of Immunoglobulin heavy chain variable region
RT (VH) gene subgroups";
RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).

CC -----


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ID      HV1G_HUMAN      STANDARD;          PRT;          117 AA.
AC      P23083;
DT      01-NOV-1991 (Rel. 20, Created)
DT      01-NOV-1991 (Rel. 20, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      IG HEAVY CHAIN V-I REGION V35 PRECURSOR.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=88295408; PubMed=2841108;
RA      Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA      Ohno H., Fukuhara S., Honjo T.;
RT      "Dispersed localization of D segments in the human immunoglobulin
RT      heavy-chain locus."
RL      EMBO J. 7:1047-1051(1988).
CC      -----
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CC      -----
DR      EMBL; X07448; -; NOT_ANNOTATED_CDS.
DR      PIR; S00476; HVH035.
DR      InterPro; IPR003006; -
DR      Pfam; PF00047; 1g; 1.
KW      Immunoglobulin V region; Signal.
FT      SIGNAL
FT      CHAIN
FT      NON_TER
FT      SEQUENCE
SQ      117 AA; 13009 MW; BE6ICE63F8CE97BD CRC64;

Query Match
Best Local Similarity 73.5%; Score 439; DB 1; Length 117;
Matches 86; Conservative 6; Mismatches 25; Indels 0; Gaps 0;

QY      1 MGWNCIIFLVTATGVSQVQVQSGAEVKKPGSSVAVSCSKAGYFTTDAIQWVQAP 60
QY      1 MDWWRILFLVAAATGASQVQVQSGAEVKKPGASVAVSCSKAGYFTTGYTMHVWVQAP 60
DB      1
DB      61 GCGLEWIGVINIYYDNTNYYNOKFKGKATMTVDKSTAYMELSLRSRSDTAVYYCAR 117
DB      61 GCGLEWIGVINIYYDNTNYYNOKFKGKATMTVDKSTAYMELSLRSRSDTAVYYCAR 117
DB      61 GCGLEWIGVINIYYDNTNYYNOKFKGKATMTVDKSTAYMELSLRSRSDTAVYYCAR 117

RESULT 13
HV49_MOUSE
ID      HV49_MOUSE      STANDARD;          PRT;          117 AA.
AC      P06328;
DT      01-JAN-1988 (Rel. 06, Created)
DT      01-JAN-1988 (Rel. 06, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      IG HEAVY CHAIN V REGION VH58 B4 PRECURSOR.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=85099340; PubMed=2578321;
RA      Yancopoulos G.D., Alt F.W.;
RT      "Developmentally controlled and tissue-specific expression of
RT      unexpressed VH gene segments."
RL      Cell 40:271-281(1985).
CC      -----
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CC      -----
DR      EMBL; M13788; AAA38506.1; -
DR      PIR; A02035; MHMSB4.
DR      InterPro; IPR003006; -
DR      Pfam; PF00047; 1g; 1.
KW      Immunoglobulin V region; Signal.
FT      SIGNAL
FT      CHAIN
FT      NON_TER
FT      SEQUENCE
SQ      117 AA; 12834 MW; B8862FAC67ABD345 CRC64;

Query Match
Best Local Similarity 60.4%; Score 435; DB 1; Length 117;
Matches 81; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY      1 MGWNCIIFLVTATGVSQVQVQSGAEVKKPGSSVAVSCSKAGYFTTDAIQWVQAP 60
QY      1 MGWNCIIFLVTATGVSQVQVQSGAEVKKPGSSVAVSCSKAGYFTTDAIQWVQAP 60
DB      1
DB      61 GCGLEWIGVINIYYDNTNYYNOKFKGKATMTVDKSTAYMELSLRSRSDTAVYYCAR 117
DB      61 GCGLEWIGVINIYYDNTNYYNOKFKGKATMTVDKSTAYMELSLRSRSDTAVYYCAR 117
DB      61 GCGLEWIGVINIYYDNTNYYNOKFKGKATMTVDKSTAYMELSLRSRSDTAVYYCAR 117

RESULT 14
HV10_MOUSE
ID      HV10_MOUSE      STANDARD;          PRT;          117 AA.
AC      P01754; P11270;
DT      21-JUL-1986 (Rel. 01, Created)
DT      01-JUL-1988 (Rel. 11, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      IG HEAVY CHAIN V REGION 145 PRECURSOR.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      STRAIN=C57BL/6;
RX      MEDLINE=81234548; PubMed=6788376;
RA      Botwell A.L.M., Pasikind M., Rech M., Imanishi-Kari T., Rajewsky K.,
RA      Baltimore D.;
RT      "Heavy chain variable region contribution to the NpB family of
RT      antibodies: somatic mutation evident in a gamma 2a variable region."
RL      Cell 24:625-637(1981).
CC      -1- MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY
CC      RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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CC      -----
DR      EMBL; J00533; AAA38602.1; -
DR      PIR; C02034; HVMS45.
DR      InterPro; IPR003006; -
DR      Pfam; PF00047; 1g; 1.
KW      Immunoglobulin V region; Signal.

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FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 145.
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT NON_TER 117 117
 SO SEQUENCE 117 AA; 12921 MW; D37DE8A3F543E996 CRC64;

Query Match

59.6%; Score 429; DB 1; Length 117;
 Best Local Similarity 69.2%; Pred. No. 3.8e-36;

Matches 81; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 1 MGNACIIFLVTATGVSOVOLVOSGAEVKPKSSSVKSCASGYFTDYAIQWRQAP 60
 DB 1 MGVSCIMFLATATGVHFOVLOQPGALVKGPAVSRLSKASGYFTSTYMHVKKRP 60
 QY 61 GQGLEWIGVINIYYDNFTYNOCKFKATMTVDKSTAYMELSLRSEDTAVYYCAR 117
 DB 61 GQGLEWIGRIDPNSGCKRYNCKFKATLTVDKPSSTAYMQLSLTSEDSAVYYCAR 117

RESULT 15

HV13_MOUSE STANDARD; PRT; 117 AA.

AC P01757;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION J558.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=80078170; PubMed=6765983;
 RA Schilling J., Clevinger B., Davie J.M., Hood L.;
 RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
 rearrangements in heavy chain V-region gene segments.";
 RL Nature 283:35-40(1980).
 CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
 BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS. MANY OF
 WHICH OCCUR IN THE D AND J SEGMENTS.
 CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
 CC PIR: A26242; MHMSJ5.
 DR InterPro: IPR003006; -
 DR Pfam: PF00047; Ig: 1.
 KW Immunoglobulin V region.
 FT DISULFID 22 96
 FT NON_TER 117 117 BY SIMILARITY.
 SO SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447EA1 CRC64;

Query Match

59.4%; Score 427.5; DB 1; Length 117;
 Best Local Similarity 70.1%; Pred. No. 5.4e-36;

Matches 82; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

QY 20 QVQVQSGAEVKKPKSSVSKVSCASGYFTDYAIQWRQAPGQGLEWIGVINIYYDNFTY 79
 DB 1 EVOLOQSGPELVKPGASVKMSCKASGYFTDYIMKWKQSHKSLKLEWIGDINPNNGGTSY 60
 QY 80 NQTKGKATMTVDKSTAYMELSLRSEDTAVYYCAR-AAWMDYWGQGLTVTVSS 135
 DB 61 NQTKGKATLTVDKSSSTAYMQLSLTSEDSAVYYCARDRYWYFDVWGAGTGVTVSS 117

Search completed: April 25, 2001, 09:40:51
 Job time: 176 sec

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OM protein - protein search, using sw model

Run on: April 25, 2001, 09:37:15 ; Search time 39.12 Seconds
(without alignments)
404.475 Million cell updates/sec

Title: US-09-249-011-6
Perfect score: 720
Sequence: 1 MGNWCIIFLVTATGVSQ.....ARAWMDYWGQCTLVTS 135

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_15:
2: sp_archaea:
3: sp_bacteria:
4: sp_fungi:
5: sp_human:
6: sp_invertebrate:
7: sp_mhc:
8: sp_mammal:
9: sp_phage:
10: sp_plant:
11: sp_rhodent:
12: sp_unclassified:
13: sp_vertebrate:
14: sp_virus:

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	454	63.1	124	4 Q9UL92	Q9UL92 homo sapien
2	441.5	61.3	119	4 Q9UL94	Q9UL94 homo sapien
3	437	60.7	116	4 Q9UL89	Q9UL89 homo sapien
4	436.5	60.6	117	11 Q9QX89	Q9QX89 mus musculu
5	432.5	60.1	150	4 Q9Y298	Q9Y298 mus musculu
6	429.5	59.7	117	11 Q9QXFO	Q9QXFO mus musculu
7	423	58.8	109	11 Q9JL75	Q9JL75 mus musculu
8	422.5	58.7	125	4 Q9UL95	Q9UL95 mus musculu
9	415.5	57.7	157	4 Q9S978	Q9S978 homo sapien
10	411	57.1	118	11 Q9Z1C4	Q9Z1C4 mus musculu
11	383	53.2	114	11 Q9JL81	Q9JL81 mus musculu
12	382	53.1	110	11 Q9JL77	Q9JL77 mus musculu
13	366.5	50.9	117	11 Q9Z1C6	Q9Z1C6 mus musculu
14	357	49.6	110	11 Q9JL83	Q9JL83 mus musculu
15	343.5	47.7	113	4 Q9UL90	Q9UL90 homo sapien
16	341.5	47.4	116	4 Q9UL93	Q9UL93 homo sapien
17	335	46.5	147	4 Q9Y509	Q9Y509 mus musculu
18	333	46.2	298	11 Q9QYFO	Q9QYFO mus musculu
19	332.5	46.2	109	11 Q9JL85	Q9JL85 mus musculu

20	322	44.7	122	4 Q9UL84	Q9UL84 homo sapien
21	320	44.4	118	4 Q9UL91	Q9UL91 homo sapien
22	317.5	44.1	121	4 Q9UL71	Q9UL71 homo sapien
23	312.5	43.4	131	4 Q9UL88	Q9UL88 homo sapien
24	307.5	42.7	102	11 Q9JL79	Q9JL79 mus musculu
25	298.5	41.5	119	4 Q9UL73	Q9UL73 homo sapien
26	298	41.2	124	6 Q9N0W4	Q9N0W4 oryctolagus
27	297	41.2	118	4 Q9UL72	Q9UL72 homo sapien
28	295	41.0	124	6 Q9N0W6	Q9N0W6 oryctolagus
29	294	40.8	437	11 Q9R1A4	Q9R1A4 mus musculu
30	280.5	39.0	112	4 Q9UGP3	Q9UGP3 homo sapien
31	279.5	38.8	104	4 Q9UL87	Q9UL87 homo sapien
32	257	35.7	150	4 Q9S973	Q9S973 mus musculu
33	252	35.0	95	4 Q9UL86	Q9UL86 homo sapien
34	246	34.2	122	4 Q9UL75	Q9UL75 homo sapien
35	234.5	32.6	121	4 Q9UL96	Q9UL96 homo sapien
36	209.5	29.1	82	4 Q9NP66	Q9NP66 homo sapien
37	205	28.5	416	4 Q9NP66	Q9NP66 homo sapien
38	204.5	28.4	76	4 Q9S742	Q9S742 mus musculu
39	193.5	26.9	82	4 Q9S725	Q9S725 mus musculu
40	192	26.7	77	4 Q9S726	Q9S726 mus musculu
41	191.5	26.6	88	4 Q9S737	Q9S737 mus musculu
42	191	26.5	80	4 Q9S727	Q9S727 mus musculu
43	189.5	26.3	118	4 Q9UL74	Q9UL74 homo sapien
44	188	26.1	77	4 Q9S728	Q9S728 mus musculu
45	187.5	26.0	79	4 Q9S731	Q9S731 mus musculu

ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	124 AA.
Q9UL92	Q9UL92			
AC	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)			
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98277139; PubMed=9614934;			
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,			
RA	Young D.C.;			
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal			
RL	fetus";			
CL	Clin. Immunol. Immunopathol. 87:184-192(1998).			
DR	EMBL; AF035022; AAD56258.1; -			
DR	INTERPRO; IPR003006; -			
DR	PFAM; PF00047; Ig; 1.			
FT	NON_TER	1	124	
FT	NON_TER	1	124	
FT	SEQUENCE	124 AA;	13580 MW;	1BAACBD96ACD2A2 CRC64;

Query Match 63.1%; Score 454; DB 4; Length 124;
Best Local Similarity 71.0%; Pred. No. 2.9e+40;
Matches 88; Conservative 13; Mismatches 15; Indels 8; Gaps 1;

QY	20	QVQVQSGAEVKKPGSSVKASGYTFDYAIDQWROAPGQGLEWIGVNIYYDNTNY	79
DB	1	EVQLVESGGGVKAPGASVSCASGYTFDYAIDQWROAPGQGLEWIGVNIYYDNTNY	60
QY	80	NKPFQKATMTVDKSTRTAYMELSSLRSEDTAVYVCARAWM-----DYWGQCTIV	131
DB	61	AKPFQKATMTVDKSTRTAYMELSSLRSEDTAVYVCARAWM-----DYWGQCTIV	120
QY	132	TVSS 135	

Db 121 TVSS 124

RESULT 2

ID 09UL94 PRELIMINARY; PRT: 119 AA.

AC 09UL94;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-JUN-2000 (TREMBLrel. 13, Last sequence update)

DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominae; Homo.

NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

RT Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RT fetus.";

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL: AF035020; AAD56256.1; -.

DR INTERPRO: IPR003006; -.

DR PFAM: PF00047; 19; 1.

FT NON_TER 1 1

FT NON_TER 119 119

FT SEQUENCE 119 AA; 13205 MW; 13E64F5345F4A16E CRC64;

Query Match

Best Local Similarity 74.2%; Score 441.5; DB 4; Length 119;

Matches 89; Conservative 8; Mismatches 18; Indels 5; Gaps 2;

QY 20 QVQLVSGAEEKRRGSSVKVSKASGTFPTDYAIQWVROAPGGLLEWIGVINYDNTNY 79

DB 1 EVQLVSGAEEKRRGSSVKVSKASGTFPTGYHNVROAPGGLLEWIGVINYDNTNY 60

QY 80 NQKFKATMTVDKSTSTAVMELSLRSEDPYAVYCARAA---WYMDYMGGLTVYSS 135

DB 61 AQRFGKAVTMTKDTISITATMELSLRSDDTAVYTCARGGGLMF-DPMGGGLTVYSS 119

RESULT 3

ID 09UL89 PRELIMINARY; PRT: 116 AA.

AC 09UL89;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-JUN-2000 (TREMBLrel. 13, Last sequence update)

DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominae; Homo.

NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

RT Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RT fetus.";

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL: AF035025; AAD56261.1; -.

DR INTERPRO: IPR003006; -.

DR PFAM: PF00047; 19; 1.

FT NON_TER 1 1

FT NON_TER 116 116

FT SEQUENCE 116 AA; 12605 MW; C8F9131DE13EAB98 CRC64;

Query Match

Best Local Similarity 60.7%; Score 437; DB 4; Length 116;

Best Local Similarity 75.0%; Pred. No. 1.6e-38;

Matches 87; Conservative 7; Mismatches 18; Indels 4; Gaps 1;

QY 24 VQSGAEVKKPGSSVKVSKASGTFPTDYAIQWVROAPGGLLEWIGVINYDNTNYQKF 83

DB 1 VQSGAEVKKPGSSVKVSKASGTFSTYALISWVQAGGGLLEWIGRIILPLGLANNAQKF 60

QY 84 KGKATMTVDKSTSTAVMELSLRSEDPYAVYCARAA---WYMDYMGGLTVYSS 135

DB 61 QGRVTITADSTSTAVMELSLRSEDPYAVYCARAA---WYMDYMGGLTVYSS 116

RESULT 4

ID 09QX9 PRELIMINARY; PRT: 117 AA.

AC 09QX9;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-JUN-2000 (TREMBLrel. 13, Last sequence update)

DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Scturognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL: AJ225174; CAB65237.1; -.

DR INTERPRO: IPR003006; -.

DR PFAM: PF00047; 19; 1.

FT NON_TER 1 1

FT NON_TER 117 117

FT SEQUENCE 117 AA; 13000 MW; CDDEZAF84D49734 CRC64;

Query Match

Best Local Similarity 60.6%; Score 436.5; DB 11; Length 117;

Matches 84; Conservative 16; Mismatches 16; Indels 1; Gaps 1;

QY 20 QVQLVSGAEEKRRGSSVKVSKASGTFPTDYAIQWVROAPGGLLEWIGVINYDNTNY 79

DB 1 EVQLVSGAEEKRRGSSVKVSKASGTFPTDYKWKVQSGGLLEWIGVINYDNTNY 60

QY 80 NQKFKATMTVDKSTSTAVMELSLRSEDPYAVYCARAAW---WYMDYMGGLTVYSS 135

DB 61 NQKFKATMTVDKSSSTATMQLNLSRSDYAVYCARADRYAMDYMGGLTVYSS 117

RESULT 5

ID 09Y298 PRELIMINARY; PRT: 150 AA.

AC 09Y298;

DT 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DE IGG VH PROTEIN PRECURSOR (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominae; Homo.

NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98322155; PubMed=9657749;

RA Jacquemin M.G., Vander Elst L.P.L.;

RT "Mechanism and kinetics of factor VII inactivation: study with an

RT IgG4 monoclonal antibody derived from a hemophilia A patient with an

RT inhibitor.";

RL Blood 92:496-506(1998).

DR EMBL: AJ224083; CA11829.1; -.

DR INTERPRO: IPR003006; -.

DR PFAM: PF00047; 19; 1.

KW Signal. 1 19 POTENTIAL.
 FT SIGNAL 150 150
 FT NON_TER 150 150
 SQ SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;

Query Match
 Best Local Similarity 60.1%; Score 432.5; DB 4; Length 150;
 Matches 86; Conservative 13; Mismatches 36; Indels 1; Gaps 1;

OY 1 MGNWCIIFLVTTATGHSQVOLVOSGAEVKRRPGSSVSKVSCASGYTFTDYAIOQVROAP 60
 DB 1 MDWTRILFLVAAATGTHAQVOLVOSGAEVKRRPGSSVSKVSCASGYTFTDYAIOQVROAP 60
 OY 61 GGGLEWIGVINYDNTNNOFKKATVTVDKSTSTAMELSLRSEDTAVYYCA-RNA 119
 DB 61 GGGLEWIGVINYDNTNNOFKKATVTVDKSTSTAMELSLRSEDTAVYYCA-RNA 119
 OY 120 WYMDYWGOGTLTVSS 135
 DB 121 DAFDIMGCTMTVSS 136

RESULT 6
 O90XF0 PRELIMINARY: PRT: 117 AA.
 AC O90XF0.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Clemens A., Rademakers A., Specht C., Koelsch E.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ225171; CAB65236.1; --
 DR INTERPRO: IPR003006; --
 DR PFM: PF00047; 19; 1.
 FT NON_TER 1 1
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;

Query Match
 Best Local Similarity 59.7%; Score 429.5; DB 11; Length 117;
 Matches 82; Conservative 17; Mismatches 17; Indels 1; Gaps 1;

OY 20 QOVQVSGAEVKKPGSSVSKVSCASGYTFTDYAIOQVROAPGQLEWIGVINYDNTNY 79
 DB 1 EVOVLQOOSGELVKKPGASVSKVSCASGYTFTDYMKWKVSHKSLIDINDPNNNGTSTY 60
 OY 80 NOKFKKATMTYDKSTSTAYMELSLRSEDTAVYYCAR-AAAYMDYWGOGTLTVSS 135
 DB 61 NOKFKKATMTYDKSTSTAYMELSLRSEDTAVYYCAR-AAAYMDYWGOGTLTVSS 117

RESULT 7
 O9JL75 PRELIMINARY: PRT: 109 AA.
 AC O9JL75.
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
 RT acetyl-glucoamine antibodies from mice with autoimmune myocarditis."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF206031; AAF69329.1; --
 FT NON_TER 1 1
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 12118 MW; FF65E441BBF936A6 CRC64;

Query Match
 Best Local Similarity 58.8%; Score 423; DB 11; Length 109;
 Matches 80; Conservative 10; Mismatches 17; Indels 2; Gaps 1;

OY 29 EVKKPGSSVSKVSCASGYTFTDYAIOQVROAPGQLEWIGVINYDNTNNOFKKAT 88
 DB 1 ELVKPGASVSKVSCASGYTFTSYVMHWKQKPGQLEWIGVINYDNTGKYNKFKKAT 60
 OY 89 MTVDKSTSTAYMELSLRSEDTAVYYCARAAW--MDYWGOGTLTVSS 135
 DB 61 LPSDKSSSTAYMELSLRSEDTAVYYCARADGNYRGFDYWGOGTLTVSS 109

RESULT 8
 O9UL95 PRELIMINARY: PRT: 125 AA.
 AC O9UL95.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-9827139; PubMed-9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL: AF035019; AAD56255.1; --
 DR INTERPRO: IPR003006; --
 DR PFM: PF00047; 19; 1.
 FT NON_TER 1 1
 FT NON_TER 125 125
 SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

Query Match
 Best Local Similarity 58.7%; Score 422.5; DB 4; Length 125;
 Matches 85; Conservative 10; Mismatches 21; Indels 9; Gaps 1;

OY 20 QOVQVSGAEVKKPGSSVSKVSCASGYTFTDYAIOQVROAPGQLEWIGVINYDNTNY 79
 DB 1 EVOVLQOOSGELVKKPGASVSKVSCASGYTFTGYMHWVROAPGQLEWIMGINDPNSGTNY 60
 OY 80 NOKFKKATMTYDKSTSTAYMELSLRSEDTAVYYCAR-----AAAYMDYWGOGTL 130
 DB 61 AOKVQGRVMTFTTSTAYMELSLRSDTAVYYCARSGGGRIAAADAFDIMGGT 120
 OY 131 VTSS 135
 DB 121 VTSS 125

RESULT 9
 O9S978 PRELIMINARY: PRT: 157 AA.
 ID O9S978

FT	NON_TER	1	1	
FT	NON_TER	110	110	
SQ	SEQUENCE	110 AA;	1213 MW;	2EDE81FB5862C9AF CRC64;

Query Match	53.1%	Score 382	DB 11	Length 110
Best Local Similarity	68.9%	Pred. No. 9.1e-33		
Matches 73	Conservative 14	Mismatches 17	Indels 2	Gaps 1

[illegible]

RESULT	13	
Q9Z1C6		
ID	Q9Z1C6	PRELIMINARY;
		PRT; 117 AA

DT	01-MAY-1999	(TREMblrel.. 10, Created)	
DT	01-MAY-1999	(TREMblrel.. 10, Last sequence update)	
DT	01-MAY-2000	(TREMblrel.. 13, Last annotation update)	
DE	ANTI-PORCINE VCAH MAB 2A2 HEAVY CHAIN VARIABLE REGION (FRAGMENT).		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
OX	NCBI_TaxId=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-BALB/C.		
RA	Mueller J.P., Giamoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,		
RA	Wells L.M., Evans M.J.		
RT	"Humanized porcine VCAH-specific monoclonal antibodies with chimeric		
RT	1992/94 constant regions block human leukocyte binding to porcine		
RT	endothelial cells."		
RL	Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: U78799; AAD00291.1; -		
DR	INTERPRO: IPR003006; -		
DR	PFAM: PF00047; Ig; 1.		
FT	NON_TER	1	
FT	NON_TER	117	1
Q0	SEQUENCE	117 AA; 13122 MW; 4F65B193AFB77E5B_CRC64;	

Query Match	50.9%	Score 366.5	DB 11	Length 117
Best Local Similarity	59.3%	Pred. No. 4.1e-31		
Matches 70; Conservative	19	Mismatches 26	Indels 3	Gaps 2

[illegible]

RESULT	14
09JL83	
ID	09JL83
AC	09JL83;
DT	01-OCT-2000 (TREMblrel. 15, Created)
DT	01-OCT-2000 (TREMblrel. 15, last sequence update)
DT	01-OCT-2000 (TREMblrel. 15, last annotation update)
DE	ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT)
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX	NCBI_TaxID=10090;
NN	[1]

RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
RL submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206023; AAF69321.1; -
FT NON_TER 1
ET 110 110
SQ SEQUENCE 110 AA; 12052 MW; 84EB6F2AD219AF95E CRC64;

Query Match	49.6%	Score 357	DB 11	Length 110
Best Local Similarity	64.2%	Pred. No. 3.8e-30		
Matches 70	Conservative 15	Mismatches 22	Indels 2	Gaps 1

Oy	29	EKKPSSSVKSSVSCAKSGYFETDVALIOWQAQGGGLEWIGVINYLYNTYNNOKRFGKAT	89
		1:	
	2	ELVAFGSAVISCASGYTFEFSNMNMWVLRGCGGLEWIGVINYLYNTYNNOKRFGKAT	61
Db			
Oy	89	MTYDKSTSTAYMELSLRSEDPAIVYICARAAM--TMDYGGGTLYTVSS	135
		1:	
Db	62	LTKAKSSIAITKQLSLTSDVSAIVFCASNDVDREFATVGGGLTVTVSA	110

RESULT	15	
Q9UL90		
ID	Q9UL90	PRELIMINARY;
		PFT;
		113 AA

DT 01-MAY-2000 (TIREMBREL. 13, Created)
DT 01-MAY-2000 (TIREMBREL. 13, last sequence update)
DT 01-JUN-2000 (TIREMBREL. 14, last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP. SEQUENCE FROM N.A.
RX MEDLINE=98271139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus".
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; 1g; 1.
FT NON_TER 1 1
FT 113 113
SO NON_TER 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match	47.7%	Score 343.5	DB 4	Length 113
Best Local Similarity	55.1%	Pred. No. 1e-28		
Matches 65	Conservative 24	Mismatches 22	Indels 7	Gaps 3

[illegible]

Search completed: April 25, 2001, 09:40:33
Job time: 198 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 25, 2001, 09:36:42 ; Search time 36.24 Seconds
(without alignments)
212.943 Million cell updates/sec

Title: US-09-249-011-6
Perfect score: 720
Sequence: 1 MGNMCIFFLVTTATGVHSQ.....ARAWMDYGGCGLVTSS 135

Scoring table:
BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues
Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
A.GeneSeq_0401.*
1: /SIDSL/gcgdata/geneseq/geneseqp/AA1980.DAT.*
2: /SIDSL/gcgdata/geneseq/geneseqp/AA1981.DAT.*
3: /SIDSL/gcgdata/geneseq/geneseqp/AA1982.DAT.*
4: /SIDSL/gcgdata/geneseq/geneseqp/AA1983.DAT.*
5: /SIDSL/gcgdata/geneseq/geneseqp/AA1984.DAT.*
6: /SIDSL/gcgdata/geneseq/geneseqp/AA1985.DAT.*
7: /SIDSL/gcgdata/geneseq/geneseqp/AA1986.DAT.*
8: /SIDSL/gcgdata/geneseq/geneseqp/AA1987.DAT.*
9: /SIDSL/gcgdata/geneseq/geneseqp/AA1988.DAT.*
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13: /SIDSL/gcgdata/geneseq/geneseqp/AA1992.DAT.*
14: /SIDSL/gcgdata/geneseq/geneseqp/AA1993.DAT.*
15: /SIDSL/gcgdata/geneseq/geneseqp/AA1994.DAT.*
16: /SIDSL/gcgdata/geneseq/geneseqp/AA1995.DAT.*
17: /SIDSL/gcgdata/geneseq/geneseqp/AA1996.DAT.*
18: /SIDSL/gcgdata/geneseq/geneseqp/AA1997.DAT.*
19: /SIDSL/gcgdata/geneseq/geneseqp/AA1998.DAT.*
20: /SIDSL/gcgdata/geneseq/geneseqp/AA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseqp/AA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseqp/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	720	100.0	135	21	B07965
2	627	87.1	135	21	B07963
3	585.5	81.3	470	21	W90935
4	582.5	80.9	470	21	W90933
5	581.5	80.8	470	21	W90934
6	579.5	80.5	470	19	W83037
7	579.5	80.5	470	21	B14779
8	579.5	80.5	470	21	W90929
9	573.5	79.7	140	15	R55556
10	567.5	78.8	470	21	W90936
11	566.5	78.7	145	19	W83038

12	566.5	78.7	145	21	B14775	Fragment of human
13	566.5	78.7	145	21	W90925	Humanised anti-Fas
14	566.5	78.7	470	19	W83036	Anti-Fas humanised
15	566.5	78.7	470	21	B14776	Humanised anti-Fas
16	566.5	78.7	470	21	W90926	Humanised HFE7A de
17	554	76.9	588	19	W71880	Anti-human Fas hum
18	554	76.9	588	21	B12917	Anti-human Fas hum
19	546	75.8	135	13	R24107	Humanised anti-Fac
20	545	75.7	135	11	R06369	Humanised anti-Fac
21	540	75.0	135	21	Y80289	Anti-Fac heavy cha
22	537	74.6	135	21	Y80288	Humanised anti-Fas
23	532	73.9	588	19	W71881	Humanised anti-Fas
24	532	73.9	588	21	B12918	Anti-human Fas hum
25	531.5	73.8	163	12	R15060	Anti-human Fas imm
26	531.5	73.8	163	12	R15200	Anti-human Fas imm
27	530.5	73.7	136	21	W77596	Anti-human Fas imm
28	530.5	73.7	140	18	W21847	Anti-human Fas imm
29	530	73.6	135	21	Y80291	Humanised heavy ch
30	530	73.6	468	13	R28808	Humanised anti-Fas
31	529.5	73.5	136	15	R59512	Sequence of the he
32	529	73.5	133	16	R81840	E-selectin CDR-gra
33	529	73.5	139	19	W36165	Humanised heavy ch
34	528.5	73.4	464	19	W83041	Anti-Fas Mab HFE7A
35	528.5	73.4	464	21	B14747	Mouse anti-Fas ant
36	528.5	73.4	464	21	W90897	Humanised anti-Fas an
37	528	73.3	137	21	Y99847	Humanised partial
38	527	73.2	135	13	R29017	pIC-Rh-1220d. Sy
39	527	73.2	139	19	W65773	Anti-human HML.24
40	527	73.2	139	20	W62205	Humanised anti-HML
41	527	73.2	139	20	Y32770	Anti-HML.24 antibo
42	527	73.2	139	20	Y02572	Humanised H chain
43	527	73.2	139	20	Y05486	H chain V region o
44	527	73.2	140	19	W77294	HML.24 antibody he
45	526	73.1	135	13	R29016	pIC-Rh-1220b. Sy

ALIGNMENTS

RESULT 1	
ID B07965	standard; Protein: 135 AA.
XX	
AC B07965;	
XX	
DT 14-NOV-2000	(first entry)
XX	
DE	A heavy chain variable region of humanised 3S1 antibody.
XX	
KW	Antibody 3S1; B7 molecule; B7; humanised immunoglobulin;
KW	autoimmune disease; infectious disease; inflammatory disorder;
KW	systemic lupus erythematosus; diabetes mellitus; insulin; asthma;
KW	arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
KW	multiple sclerosis; transplant rejection; proliferative disease;
KW	leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
KW	aplastic anaemia; myeloid dysplasia syndrome.
XX	
OS Synthetic.	
OS Mus sp.	
OS Homo sapiens.	
XX	
FH	Key
FT Peptide	1..19
FT	/note= "signal peptide"
FT Protein	20..135
FT	/note= "mature protein"
FT Region	50..54
FT	/note= "complementarity determining region 1"
FT Region	69..85
FT	/note= "complementarity determining region 2"
FT Region	118..124
FT	/note= "complementarity determining region 3"
XX	

PN W0200047625-A2.
 XX 17-AUG-2000.
 XX
 PE 09-FEB-2000: 2000MCO-US03303.
 XX
 PR 12-FEB-1999: 990S-0249011.
 PR 24-JUN-1999: 990S-0339596.
 XX
 PA (GEMV) GENETICS INST INC.
 XX
 PI Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;
 PI Gray GS, Knight A, O'hara D, Rup B, Veldman GW;
 XX
 DR WPI: 2000-524532/47.
 DR N-PSDB: A59694.
 XX
 PT Humanized immunoglobulin having a binding specificity to B7-1 (derived
 PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,
 PT modulates immune responses and can therefore treat e.g. autoimmune
 PT diseases, infectious diseases -
 XX
 PS Example 3: Fig 2A; 162pp; English.
 XX
 CC The present sequence represents the heavy chain variable region
 CC of the humanised murine antibody 3D1. The antibody has a binding
 CC specificity to B7 molecules. The antibody is used to construct humanized
 CC immunoglobulins, which comprise an antigen binding region of non-human
 CC origin and a portion of a human immunoglobulin. The humanized
 CC immunoglobulins are useful for treating autoimmune diseases, infectious
 CC diseases, inflammatory disorders, systemic lupus erythematosus, diabetes
 CC mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease,
 CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are
 CC also useful for treating a transplant recipient or preventing transplant
 CC rejection in a transplant recipient, and treating proliferative disease
 CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,
 CC thalassemia and aplastic anaemia), inborn errors of metabolism,
 CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
 CC
 XX
 SQ Sequence 135 AA;
 QY 1 MGNWCIIFLVTATGVSQVLQVSGAEVKKPSSSVKSCASGYFTPTDAIOMVRQAP 60
 Db 1 mgwncilfflvtatgvsqvlvsgaevkkpsssvkscasgyfttqdaiqwvrgap 60
 QY 61 GGGLEWIGVINIYYDNTNYNOKFKGKATWVDKSTAYMELSLRSEDYAVYYCARAAW 120
 Db 61 ggglewigvinilydntnynokfkakatwvdksstaymelslrsedyavycaraaw 120
 QY 121 YMDYWGQGLTWTSS 135
 Db 121 ymdywgqglwtvss 135
 RESULT 2
 B07963
 ID B07963 standard: Protein: 135 AA.
 XX
 AC B07963;
 XX
 DT 14-NOV-2000 (first entry)
 XX
 DE Amino acid sequence of heavy chain variable region of 351 antibody.
 XX
 KM Antibody 3D1: B7 molecule; B7: humanised immunoglobulin;
 KM autoimmune disease; infectious disease; inflammatory disorder;
 KM systemic lupus erythematosus; diabetes mellitus; insulinitis; asthma;
 KM arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
 KM

KM multiple sclerosis; transplant rejection; proliferative disease;
 KM leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
 KM aplastic anaemia; myeloid dysplasia syndrome.
 XX
 OS Mus sp.
 XX
 FH Key
 FT Peptide
 FT
 FT Location/Qualifiers
 FT 1..19
 FT /note= "signal peptide"
 FT 20..135
 FT Protein
 FT /note= "mature protein"
 FT 50..54
 FT /note= "complementarity determining region 1"
 FT 69..85
 FT /note= "complementarity determining region 2"
 FT 118..124
 FT /note= "complementarity determining region 3"
 XX
 XX W0200047625-A2.
 XX 17-AUG-2000.
 XX
 PE 09-FEB-2000: 2000MCO-US03303.
 XX
 PR 12-FEB-1999: 990S-0249011.
 PR 24-JUN-1999: 990S-0339596.
 XX
 PA (GEMV) GENETICS INST INC.
 XX
 PI Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;
 PI Gray GS, Knight A, O'hara D, Rup B, Veldman GW;
 XX
 DR WPI: 2000-524532/47.
 DR N-PSDB: A59692.
 XX
 PT Humanized immunoglobulin having a binding specificity to B7-1 (derived
 PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,
 PT modulates immune responses and can therefore treat e.g. autoimmune
 PT diseases, infectious diseases -
 XX
 PS Example 1: Fig 1A; 162pp; English.
 XX
 CC The present sequence represents the heavy chain variable region of the
 CC murine antibody 3D1. The antibody has a binding specificity to B7
 CC molecules. The antibody is used to construct humanized immunoglobulins,
 CC which comprise an antigen binding region of non-human origin and a
 CC portion of a human immunoglobulin. The humanized immunoglobulins are
 CC useful for treating autoimmune diseases, infectious diseases,
 CC inflammatory disorders, systemic lupus erythematosus, diabetes
 CC mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease,
 CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are
 CC also useful for treating a transplant recipient or preventing transplant
 CC rejection in a transplant recipient, and treating proliferative disease
 CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,
 CC thalassemia and aplastic anaemia), inborn errors of metabolism,
 CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
 CC
 XX
 SQ Sequence 135 AA;
 QY 1 MGNWCIIFLVTATGVSQVLQVSGAEVKKPSSSVKSCASGYFTPTDAIOMVRQAP 60
 Db 1 mgwncilfflvtatgvsqvlvsgaevkkpsssvkscasgyfttqdaiqwvrgap 60
 QY 61 GGGLEWIGVINIYYDNTNYNOKFKGKATWVDKSTAYMELSLRSEDYAVYYCARAAW 120
 Db 61 ggglewigvinilydntnynokfkakatwvdksstaymelslrsedyavycaraaw 120
 QY 121 YMDYWGQGLTWTSS 135
 Db 121 ymdywgqglwtvss 135
 Query Match 87.18; Score 627; DB 21; Length 135;
 Best Local Similarity 84.48; Pred. No. 2,4e-47;
 Matches 114; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

CC The invention relates to compositions for the prevention or treatment
 CC of diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanized version of HFE7A containing identical CDRs
 CC (complementarily determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The compositions of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. Sequences B14775-B14776 and B14779
 CC represent the heavy chains (or fragments thereof) of various humanised
 CC HFE7A-derived anti-Fas antibodies.
 CC
 SQ Sequence 470 AA:
 Query Match 80.5% ; Score 579.5; DB 21; Length 470;
 Best Local Similarity 80.0% ; Pred. No. 1.1e-42;
 Matches 112; Conservative 8; Mismatches 15; Indels 5; Gaps 1;
 QY 1 MGNWCIIFLVTATGHSQVQLVQSGAEVKKRPGSSSVKVSCKASGYFTDTAIDWRQAP 60
 Db 1 MGNWCIIFLVTATGHSQVQLVQSGAEVKKRPGSSSVKVSCKASGYFTDTAIDWRQAP 60
 QY 61 GQGLEWIGVINYDNTNRYNOKFKGKATMYDKSTAYAMELSSLRSDPAVYYCARAA- 119
 Db 61 GQGLEWIGVINYDNTNRYNOKFKGKATMYDKSTAYAMELSSLRSDPAVYYCARAA- 119
 QY 120 ---WYMDYWGQGLTVTVSS 135
 Db 121 YSNWYFDVWGEGLTVTVSS 140
 RESULT 8
 W90929
 ID W90929 standard; Protein: 470 AA.
 AC W90929;
 XX
 DT 08-AUG-2000 (first entry)
 DE Humanised HFE7A designed heavy chain protein #2.
 XX
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antileukemic; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto's disease; rheumatoid arthritis; graft versus host disease;
 KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; steatitis; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia; purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomypathy; glomerulonephritis; hepatitis; transplant rejection.
 XX
 OS Synthetic.
 XX
 PN EP990663-A2.
 PD 05-APR-2000.
 XX
 PF 29-SEP-1999; 99EP-0307711.
 XX
 PR 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX
 PA (\$ANY) SANKYO CO LTD.
 PI Setiawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 DR WPI; 2000-258930/23.

DR N-PSDB; A11622.
 XX
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems
 XX
 PS Example reference 22; Page 150-152; 263pp; English.
 XX
 CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antileukemic, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus-erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia, purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A designed heavy chain which is used in
 CC the method described in the invention.
 XX
 SQ Sequence 470 AA:
 Query Match 80.5% ; Score 579.5; DB 21; Length 470;
 Best Local Similarity 80.0% ; Pred. No. 1.1e-42;
 Matches 112; Conservative 8; Mismatches 15; Indels 5; Gaps 1;
 QY 1 MGNWCIIFLVTATGHSQVQLVQSGAEVKKRPGSSSVKVSCKASGYFTDTAIDWRQAP 60
 Db 1 MGNWCIIFLVTATGHSQVQLVQSGAEVKKRPGSSSVKVSCKASGYFTDTAIDWRQAP 60
 QY 61 GQGLEWIGVINYDNTNRYNOKFKGKATMYDKSTAYAMELSSLRSDPAVYYCARAA- 119
 Db 61 GQGLEWIGVINYDNTNRYNOKFKGKATMYDKSTAYAMELSSLRSDPAVYYCARAA- 119
 QY 120 ---WYMDYWGQGLTVTVSS 135
 Db 121 YSNWYFDVWGEGLTVTVSS 140
 RESULT 9
 R55556
 ID R55556 standard; Protein: 140 AA.
 AC R55556;
 XX
 DT 16-NOV-1994 (first entry)
 DE DREG-200 Humanized antibody heavy chain variable region.
 XX
 KW DREG-200; L-selectin; LECAM-1; Mel-14; LAM-1;
 KW humanized antibody; immunoglobulin; Ig; IgG1; IgG4;
 KW complementarity determining region; CDR; monoclonal antibody; Mab;
 KW framework; light chain; heavy chain; variable domain;
 KW monoclonal antibody; acceptor antibody Eu; transgenic animal.
 XX
 OS Mus sp.; Homo sapiens.

XX Key Location/Qualifiers
FH Peptide 1.19
FT Region /label-Sig-peptide
FT Region 50..54
FT Region /label-CDR1
FT Region 69..85
FT Region /label-CDR2
FT Region 118..129
FT Region /label-CDR3
XX W09412215-A.
XX 09-JUN-1994.
XX 30-NOV-1993; 93WO-US11612.
XX 01-DEC-1992; 92US-0983946.
XX (PROT-) PROTEIN DESIGN LABS INC.
XX Co MS:
XX WPI: 1994-199974/24.
XX N-PSDB: Q66702.
XX New humanised antibody specific for L-selectin - with murine CDR
PT and human framework regions, inhibits binding of neutrophils to
PT endothelial cells and useful for treating or preventing
PT inflammation
XX Disclosure: Fig. 3B; 60pp; English.
XX An L-selectin-specific IgG1 or IgG4 humanized antibody has CDRs
CC corresponding to those of mouse Mab DREG-200 and heavy and light
CC chain variable region frameworks of the human acceptor antibody Eu.
CC Nucleotide and aa sequences are provided for the DREG-200 light
CC (Q66702) and heavy (Q66700, R55554) chain variable regions
CC and the humanized DREG-200 light (Q66701, R55555) and heavy (Q66702,
CC R55556) chain variable regions. The humanized antibodies can be
CC produced economically in large quantities by expression in mammalian
CC cell culture or in transgenic animals.
XX Sequence 140 AA:
SQ
Query Match 79.7%; Score 573.5; DB 15; Length 140;
Best Local Similarity 78.6%; Pred. No. 1.1e-42;
Matches 110; Conservative 8; Mismatches 17; Indels 5; Gaps 1;
OY 1 MGNMCIIFLVTATGVSQVLOVSGAEVKKPGSSVKASCASGTTFTDAIOMWRAP 60
DB 1 mgnsciliflvtatgvsqvlvsgaevkpgssvkvscasgyltlyymhvrqap 60
OY 61 GCGLEMGIVINYYNTNYSNOKFKATPTVSKSTAVMEJLSRSEPTAVYYCARAAW 120
DB 61 ggglewiyiyipyndgtkynefkgrvtltsdestntatymejlsrseetavyycaarey 120
OY 121 ----YMDYWGQGLVTVSS 135
DB 121 gnyvryfdwgggltlvtrss 140
RESULT 10
W90936 W90936 standard; Protein: 470 AA.
XX AC W90936:
XX 08-AUG-2000 (first entry)
XX Humanised HFE7A designed heavy chain HHH type protein.
XX

KM Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KM anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiac;
KM dermatological; immunosuppressive; thymometric; antirheumatic; anti-Fas;
KM neoprotective; antinfertility; neuroprotective; antiarteriosclerotic;
KM hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KM Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KM Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
KM Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KM multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KM insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KM cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX Synthetic.
XX EP930663-A2.
XX 05-APR-2000.
XX 29-SEP-1999; 99EP-0307711.
XX 30-SEP-1998; 98JP-0276881.
XX 30-SEP-1998; 98JP-0276882.
XX (SANY) SANKYO CO LTD.
XX Serizawa N, Haryama H, Nakahara K, Tamaki I, Takahashi T;
XX WPI: 2000-258930/23.
XX N-PSDB: A11655.
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems
XX Claim 2; Page 188-189; 263pp; English.
XX This invention describes a novel humanized anti-Fas antibody-like
XX molecule (I) that induces apoptosis in cells with an abnormal Fas/Fas
XX ligand system, by binding to Fas on the cell surface, and prevents
XX apoptosis in cells with a normal system, by inhibiting binding between
XX Fas and its ligand. The products of the invention have anti-inflammatory,
XX anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
XX immunomodulatory, dermatological, immunosuppressive, thymometric,
XX antirheumatic, neoprotective, antinfertility, neuroprotective,
XX antiarteriosclerotic, cardiac and hepatropic activity. (I) induce
XX apoptosis by binding to cell surface Fas or inhibit it by competitive
XX inhibition of ligand binding. (I) are used to treat and/or prevent
XX diseases associated with the Fas/Fas ligand system, especially systemic
XX lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
XX versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
XX anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
XX disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
XX multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
XX dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
XX cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
XX (B, C or D) or alcoholol), and transplant rejection. (I) selectively
XX inhibit apoptosis in normal cells but selectively induce it in abnormal
XX cells. They bind to both human and murine Fas, so can be evaluated in
XX murine disease models. (I) act on the active site of Fas, i.e. they mimic
XX the native ligand, do not induce liver disease, and have reduced risk of
XX inducing a human anti-murine antibody response. This sequence represents
XX a humanised anti-Fas antibody HFE7A heavy chain construct HHH type
XX which is described in the method of the invention.
SQ Sequence 470 AA:
Query Match 78.8%; Score 567.5; DB 21; Length 470;
Best Local Similarity 78.6%; Pred. No. 1.3e-41;
Matches 110; Conservative 8; Mismatches 17; Indels 5; Gaps 1;
OY 1 MGNMCIIFLVTATGVSQVLOVSGAEVKKPGSSVKASCASGTTFTDAIOMWRAP 60
DB 1 mgnsciliflvtatgvsqvlvsgaevkpgssvkvscasgyltlyymhvrqap 60

Db	1	mgwscilflfvatalcylhnsqqlvqsgaevkkipasvkveackasyflfcsymmgwvtrgap	60
Qy	61	CGGLEMGICVITVINDNNYKNCKFEKGKATMYDKSTSTAYNELSLREEDTAVYICARAA- 119	
Db	61	gggleimgelipsdsyltrngkifgyrvltldtstslaymelslrqedavycarnrd	120
Qy	120	----WYMDYMGCGTLWVSS 135	
Db	121	ysnmwyfdvngwgeglvtrvss 140	
RESULT	11		
W83038			
AC	W83038	standard; Protein; 145 AA.	
XX	W83038:		
DT	15-MAR-1999	(first entry)	
XX			
DE	Anti-Fas humanised antibody HFE7A heavy chain variable region.		
XX			
KW	HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;		
KW	apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;		
KW	systemic lupus erythematosus; graft versus host disease;		
KW	Sjogren syndrome; pernicious anaemia; Addison's disease;		
KW	scleroderma; Goodpasture syndrome; Crohn's disease; sterility;		
KW	rheumatoid arthritis; autoimmune haemolytic anaemia;		
KW	myasthenia gravis; multiple sclerosis; Basedow's disease;		
KW	thrombopenia purpura; insulin-dependent diabetes; allergy;		
KW	atopy; arteriosclerosis; myocarditis; cardiomyopathy;		
KW	glomerular nephritis; hypoparathyroidism; hepatitis; AIDS;		
KW	transplant rejection; therapy.		
XX			
OS	Homo sapiens.		
OS	Synthetic.		
XX			
EH	Key	Location/Qualifiers	
FT	Peptide	1..19	
FT		/label= sig_peptide	
FT	Protein	20..145	
FT		/label= Mat_protein	
FT	Region	50..54	
FT		/label= CDR_H1	
FT	Region	/note= "claim 9"	
FT		69..84	
FT	Region	/label= CDR_H2	
FT		/note= "claim 9"	
FT	Region	118..129	
FT		/label= CDR_H3	
FT		/note= "claim 9"	
XX			
XX	AU9859701-A.		
XX			
XX	08-OCT-1998.		
XX			
PF	30-MAR-1998:	98AU-0059701.	
XX			
PR	08-OCT-1997:	97JP-0276064.	
PR	01-APR-1997:	97JP-0082953.	
PR	25-JUN-1997:	97JP-0169088.	
XX			
XX	(SANY) SANKYO CO LTD.		
XX			
PI	AKIO S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;		
PI	Masahiko O, Nobufusa S, Shun Y, Yohru T;		
XX			
DR	WPI: 1998-543440/47.		
DR	N-PSDB: V70104.		
PT			
PT	New antibodies and proteins bind conserved epitope of Fas antigen -		
PT	used to evaluate drugs in animal models and to treat Fas-associated		
PT	diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,		
PT	myocarditis, hepatitis and AIDS		

XX	Example 3: Page 207; 292pp: English.	
PS		
CC	This is the amino acid sequence of the VD type humanised heavy	
CC	chain variable region of murine anti-human Fas monoclonal antibody	
CC	HEF7A. It was utilised in a claimed humanised HEF7A heavy chain	
CC	(see V70079). The invention provides methods for producing humanised	
CC	antibodies by culturing host cells. Humanised versions of HEF7A (see	
CC	W83031-37) are capable of inducing apoptosis in abnormal cells	
CC	expressing Fas, and of inhibiting Fas-induced apoptosis in normal	
CC	cells. Humanised antibodies are used to evaluate, in animal models,	
CC	treatments of diseases that involve Fas/Fas ligand interactions, and	
CC	also to treat such diseases, including autoimmune disease (e.g.	
CC	systemic lupus erythematosus, Hashimoto's disease, graft versus host	
CC	disease, Sjogren syndrome, pernicious anaemia, Addison's disease,	
CC	scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid	
CC	arthritis, autoimmune haemolytic anaemia, sterility, myasthenia	
CC	gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura	
CC	and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,	
CC	myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic	
CC	anaemia, hepatitis, AIDS and transplant rejection (all claimed).	
XX		
XX	Sequence 145 AA;	
SO		
Query Match	78.7%; Score 566.5; DB 19; Length 145;	
Best Local Similarity	78.6%; Pred. No. 4.5e-42;	
Matches 110; Conservative	8; Mismatches 17; Indels 5; Gaps 1;	
QY	1 MGNMCIFFLVYTTATGCHSQVOLVOSGAEVKKPGSSVAVKSKASGYRTTDAIOWKQAP 60	
Db	1 mgwscilflflvalatqyhsqqlvsgsgaevkkpgasvkvskasgytltsymmwvkvqap 60	
QY	61 GGGLEIVIVINYYDNTNYNOKFKGAKMTYDKSTPTMYELSSLRSDPTAVYVCARAA- 119	
Db	61 gqrlwmeigepdsdytnyngkfkgkaltylvtasastaymelslrseadtavyycarnrd 120	
QY	120 ---WYMDYWGCGTLVTVSS 135	
Db	121 ysmnyfdwvgegtlvtvss 140	
RESULT 12		
BI4775	BI4775 standard; peptide; 145 AA.	
XX	BI4775;	
XX	24-NOV-2000 (first entry)	
DE	Fragment of humanised anti-Fas antibody heavy chain, SEQ ID NO:75.	
XX		
XX	Anti-Fas antibody; monoclonal antibody HEF7A; FERM-BP-5828;	
KW	murine; humanised antibody; complementarily determining region; CDR;	
KW	human Fas; Fas ligand; apoptosis modulator; programmed cell death;	
KW	autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;	
KW	cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;	
KW	hepatitis; AIDS; graft rejection; heavy chain.	
OS	Chimeric - Mus musculus.	
OS	Chimeric - Homo sapiens.	
XX		
PN	JP2000169393-A.	
XX		
PD	20-JUN-2000.	
XX		
PF	30-SEP-1999; 99JP-0278301.	
XX		
PR	30-SEP-1998; 98JP-0276883.	
XX		
XX	(SANY) SANKYO CO LTD.	
XX		
XX	WPI: 2000-485645/43.	
XX		

DR N-PSDB: A72146.

XX Preventive or treating agent for the diseases caused by an abnormality
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody

PS Example 15; Page 88; 139pp; Japanese.

XX The invention relates to compositions for the prevention or treatment
 CC or diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The compositions of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. Sequences B1475-B1476 and B14779
 CC represent the heavy chains (or fragments thereof) of various humanised
 CC HFE7A-derived anti-Fas antibodies.

XX Sequence 145 AA;

SO Query Match 78.7%; Score 566.5; DB 21; Length 145;
 Best Local Similarity 78.6%; Pred. No. 4.5e-42;
 Matches 110; Conservative 8; Mismatches 17; Indels 5; Gaps 1;

OY 1 MGNMCIIFLVTTATGCHSOVOIVSGAEVKKRPGSSVKVSKASGTYTFDYAIOWVRAP 60

DB 1 MGWSCHILFLVATATGCHSOVOIVSGAEVKKRPGASVKKSCASGYTLFSYMWGVKQAP 60

OY 61 GGGLEWIGVINIYDNTNNOFKKATMTVDKSTSTAYMELSLRSEPTAVYYCARAA- 119

DB 61 GGRLEWIGELDPSDSTYNGKFKKATLTVDLSASTAYMELSLRSEDATVYYCAARN 120

OY 120 ---WTMDYWGQGTIVTVSS 135

DB 121 YSNWYFDWVGEGTLTVSS 140

DE RESULT 13

W90925 ID W90925 standard; Protein: 145 AA.

AC W90925;

DT 08-AUG-2000 (first entry)

XX Humanised anti-Fas antibody HFE7A heavy chain protein.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
 KW dermatological; immunosuppressive; thyromimetic; antihematitic; anti-Fas;
 KW nephrotropic; antinfertility; neuroprotective; antiatherosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombocytopenia; purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

OS Synthetic.

PN EP990663-A2.

XX 05-APR-2000.

XX 29-SEP-1999; 99EP-0307711.

PR 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.

XX (SANY) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

XX WPI: 2000-258930/23.

DR N-PSDB: A11584.

PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems

PS Example reference 15; Page 126-127; 263pp; English.

XX This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiac and hepatotropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombocytopenia, purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A heavy chain which is used in
 CC the method described in the invention.

SO Sequence 145 AA;

Query Match 78.7%; Score 566.5; DB 21; Length 145;
 Best Local Similarity 78.6%; Pred. No. 4.5e-42;
 Matches 110; Conservative 8; Mismatches 17; Indels 5; Gaps 1;

OY 1 MGNMCIIFLVTTATGCHSOVOIVSGAEVKKRPGSSVKVSKASGTYTFDYAIOWVRAP 60

DB 1 MGWSCHILFLVATATGCHSOVOIVSGAEVKKRPGASVKKSCASGYTLFSYMWGVKQAP 60

OY 61 GGGLEWIGVINIYDNTNNOFKKATMTVDKSTSTAYMELSLRSEPTAVYYCARAA- 119

DB 61 GGRLEWIGELDPSDSTYNGKFKKATLTVDLSASTAYMELSLRSEDATVYYCAARN 120

OY 120 ---WTMDYWGQGTIVTVSS 135

DB 121 YSNWYFDWVGEGTLTVSS 140

DE RESULT 14

W83036 ID W83036 standard; Protein: 470 AA.

AC W83036;

XX 15-MAR-1999 (first entry)

XX Anti-Fas humanised antibody HFE7A heavy chain.

XX HFE7A: monoclonal antibody; mouse; Fas; humanised antibody;
 KW aplolysis; HFE7A: autoimmune disease; Hashimoto's disease;
 KW Sjogren syndrome; perniciolous anaemia; Addison's disease;
 KW Sjogren syndrome; perniciolous anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KM transplant rejection; therapy.
 XX Homo sapiens.
 OS Synthetic.
 XX
 FH Key
 FT Peptide
 FT 1..19
 FT /label= Sig-peptide
 FT Protein
 FT 20..470
 FT /label= Mat-protein
 FT Region
 FT 20..140
 FT /label= Variable
 FT Region
 FT 141..464
 FT /label= Constant
 FT Region
 FT 50..54
 FT /label= CDR_H1
 FT /note= "claim 9"
 FT Region
 FT 69..84
 FT /label= CDR_H2
 FT /note= "claim 9"
 FT Region
 FT 118..129
 FT /label= CDR_H3
 FT /note= "claim 9"
 FT Region
 FT 118..129
 FT /label= CDR_H3
 FT /note= "claim 9"
 XX
 PN AU859701-A.
 XX
 PD 08-OCT-1998.
 XX
 PF 30-MAR-1998: 98AU-0059701.
 XX
 PR 08-OCT-1997: 97JP-0276064.
 PR 01-APR-1997: 97JP-0082953.
 PR 25-JUN-1997: 97JP-0169088.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 PI Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX
 DR WPI: 1998-543440/47.
 DR N-PSDB: V70079.
 XX
 PT New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX
 PS Claim 22: Page 212-213; 292pp; English.
 XX
 CC This is the amino acid sequence of the VD type humanised heavy
 CC chain of murine anti-human Fas monoclonal antibody HFE7A. E. coli
 CC pGHS17A62 SANK 73397 harbors plasmid pGHS17A62 carrying a fusion
 CC fragment of the humanised VD type HFE7A heavy chain and DNA
 CC encoding human IgG1 constant region (see V70079), and is deposited
 CC as FERM-BP-6074 (claimed). The invention provides methods for
 CC producing humanised antibodies by culturing host cells. Humanised
 CC versions of HFE7A (see W83031-37), like native HFE7A, are capable
 CC of inducing apoptosis in abnormal cells expressing Fas, and of
 CC inhibiting Fas-induced apoptosis in normal cells. The humanised
 CC antibodies are used to evaluate, in animal models, treatments of
 CC diseases that involve Fas/Fas ligand interactions, and also to
 CC treat such diseases, including autoimmune disease (e.g. systemic

CC lupus erythematosus; Hashimoto's disease, graft versus host disease,
 CC Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,
 CC Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,
 CC autoimmune haemolytic anaemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura and
 CC insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
 CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
 CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
 XX
 SQ Sequence 470 AA:
 Query Match 78.7%; Score 566.5; DB 19; Length 470;
 Best Local Similarity 78.6%; Pred. No. 1.5e-41;
 Matches 110; Conservative 8; Mismatches 17; Indels 5; Gaps 1;
 QY 1 MGNACITFLVTTATGHSQVQLVQSGAEYFKRGSVKVCSKASGTFITDAIOWNQAP 60
 DB 1 MGVSCILIFVATATGHSQVQLVQSGAEYFKRGSVKVCSKASGTFITDAIOWNQAP 60
 QY 61 GQGLEWIGVNIYVDNNTNYNOKFKRATMTYDKSTRAVVELSLRSEDPAAVYCARAA- 119
 DB 61 GRLTMMGEIDPSQSYLNQKFKGKATLVDSASTAYMEISLSRDEATVYCARND 120
 QY 120 ---WYMDYWGQGTITVSS 135
 DB 121 YSNMWFDFVWGEGLTVLSS 140
 RESULT 15
 B14776
 ID B14776 standard; Protein: 470 AA.
 XX
 AC B14776;
 XX
 DT 24-NOV-2000 (first entry)
 XX
 DE Humanised anti-Fas antibody heavy chain, SEQ ID NO:89.
 XX
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; humanised antibody; complementarity determining region; CDR;
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerular nephritis; aplastic anaemia; pancytopenias;
 KW hepatitis; AIDS; graft rejection; heavy chain.
 XX
 OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX
 PN JP2000169393-A.
 XX
 PD 20-JUN-2000.
 XX
 PF 30-SEP-1999: 99JP-0278301.
 XX
 PR 30-SEP-1998: 98JP-0276883.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 PI WPI: 2000-485645/43;
 PI N-PSDB: A72159.
 XX
 PT Preventive or treating agent for the diseases caused by an abnormality
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody
 XX
 PS Claim 21: Page 95-96; 139pp; Japanese.
 XX
 CC The invention relates to compositions for the prevention or treatment
 CC of diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs

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OM protein - protein search, using sw model

Run on: April 25, 2001, 09:36:42 ; Search time 20.89 Seconds

(without alignments)
124.149 Million cell updates/sec

Title: US-09-249-011-6

Perfect score: 720
Sequence: 1 MGNMCIFFLVTTATGVHSQ.....APAAWMDYWGQGLTVTVSS 135

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued_Patents_AA:*

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2: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCROS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	573.5	79.7	140	US-08-579-378A-12	Sequence 12, Appl
2	573.5	79.7	140	PCT-US93-11612-12	Sequence 12, Appl
3	545	75.7	135	US-07-634-278-19	Sequence 19, Appl
4	545	75.7	135	US-08-477-728-19	Sequence 19, Appl
5	545	75.7	135	US-08-474-040-19	Sequence 19, Appl
6	545	75.7	135	US-08-487-200-19	Sequence 19, Appl
7	545	75.7	135	US-08-303-569B-31	Sequence 31, Appl
8	545	75.7	135	US-08-484-537-19	Sequence 19, Appl
9	531.5	73.8	163	PCT-US91-02942-5	Sequence 5, Appl
10	530.5	73.7	140	US-08-836-561-63	Sequence 63, Appl
11	530	73.6	467	US-07-916-098A-45	Sequence 45, Appl
12	529.5	73.5	136	PCT-US93-11611-11	Sequence 11, Appl
13	529.5	73.5	136	US-08-513-968-44	Sequence 44, Appl
14	529	73.5	139	US-08-656-586-8	Sequence 8, Appl
15	527	73.2	135	US-08-137-117D-102	Sequence 102, Appl
16	527	73.2	135	US-08-436-717-102	Sequence 102, Appl
17	526	73.1	133	US-08-718-323A-8	Sequence 8, Appl
18	525	72.9	139	US-08-253-877C-19	Sequence 19, Appl
19	525	72.9	139	US-08-452-164A-19	Sequence 19, Appl
20	525	72.9	139	US-08-603-024-18	Sequence 18, Appl
21	521	72.4	135	US-08-137-117D-100	Sequence 100, Appl
22	521	72.4	135	US-08-436-717-100	Sequence 100, Appl
23	521	72.4	137	US-08-513-968-38	Sequence 38, Appl
24	518.5	72.0	140	US-08-836-561-74	Sequence 74, Appl
25	515.5	71.6	140	US-08-836-561-78	Sequence 78, Appl
26	515	71.5	135	US-08-137-117D-112	Sequence 112, Appl
27	515	71.5	135	US-08-436-717-112	Sequence 112, Appl

28	508.5	70.6	143	US-08-236-520-7	Sequence 7, Appl
29	508.5	70.6	143	PCT-US95-05262-7	Sequence 7, Appl
30	507.5	70.5	140	US-08-836-561-83	Sequence 83, Appl
31	503.5	69.9	140	US-07-946-421-28	Sequence 28, Appl
32	501.5	69.7	123	US-08-482-882-53	Sequence 53, Appl
33	501.5	69.7	123	US-08-483-389-53	Sequence 53, Appl
34	501.5	69.7	123	US-08-487-113D-53	Sequence 53, Appl
35	501.5	69.7	123	US-08-473-503-53	Sequence 53, Appl
36	501.5	69.7	123	US-08-483-932-53	Sequence 53, Appl
37	501.5	69.7	123	US-08-720-420A-53	Sequence 53, Appl
38	501.5	69.7	123	US-08-714-017-53	Sequence 53, Appl
39	501.5	69.7	123	US-08-475-680-53	Sequence 53, Appl
40	500.5	69.5	142	US-08-476-176B-14	Sequence 14, Appl
41	500.5	69.5	142	US-08-127-721A-14	Sequence 14, Appl
42	500.5	69.5	142	US-08-485-246A-14	Sequence 14, Appl
43	499	69.3	128	US-09-199-148-57	Sequence 12, Appl
44	498	69.2	116	US-07-634-278-57	Sequence 57, Appl
45	498	69.2	116	US-07-634-278-73	Sequence 73, Appl

ALIGNMENTS

RESULT 1
US-08-579-378A-12
Sequence 12, Application US/08579378A
Patent No. 6210671
GENERAL INFORMATION:
APPLICANT: CO, Man Sung
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OR INVENTION: L-Selectin
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/579,378A
FILING DATE: 27-DEC-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/160,074
FILING DATE: 30-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95112895.8
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95114696.8
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheit, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 11823-002220
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-579-378A-12

Query Match	79.78;	Score 573.5;	DB 4;	Length 140;
Best Local Similarity	78.68;	Pred. No. 2.9e-50;		
Matches 110; Conservative	8;	Mismatches 17;	Indels 5;	Gaps 1;

[illegible]

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: RESULT      2
: PCT-US93-11612-12
: Sequence 12, Application PC/TUS9311612
: GENERAL INFORMATION:
: APPLICANT: Co, Man Sung
: TITLE OF INVENTION: Humanized Antibodies Reactive with
: TITLE OF INVENTION: L-Selectin
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourie and Crew
: STREET: One Market Plaza, Steuart Tower, Suite 2000
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: Zip: 94105
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/11612
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/983,946
: FILING DATE: 01-DEC-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, William M.
: REGISTRATION NUMBER: 30,223
: REFERENCE/DOCKET NUMBER: 11623-22
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-326-2400
: TELEFAX: 415-326-2422
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 140 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: PCT-US93-11612-12

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Query Match      79.7%; Score 573.5; DB 5; Length 140;
Best Local Similarity 78.6%; Pred. No.2.9e-50;
Matches 110; Conservative 8; Mismatches 17; Indels 5; Gaps 1;

QY      1 MGNMCIIFELTTATGVSQVQLVDSGAIEVKKPGSSVYVSKASCAYTFETDVAIQWVROP 60
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Db      1 MGNMCIIFELVATATGVSQVQLVDSGAIEVKKPGSSVYVSKASCAYTFTSYVMHNVROP 60
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QY      61 GCGLEMGVINYINDNTNINOKFKGATMTYDKSTSTAMELSSRSEDTAVYTCARAAW 120
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D_b 61 GQGLEMIGIYIPNDYSGFRYNKEFKGRGRTITSDESTNIAVHLSLRBEDPAIVYICAREEY 120
Q_y 121 -----YMDYWGQGTLLVTVSS 135
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D_b 121 GNYYRYFDVMQGQTLLVTVSS 140

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RESULT 3
US-07-634-278-19
Sequence 19, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINCH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
type: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-634-278-19

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Query Match	75.78;	Score 545;	DB 1;	Length 135;
Best Local Similarity	77.88;	Pred. NO. 2e-47;		
Matches 105; Conservative	7;	Mismatches 23;	Indels 0;	Gaps 0

[illegible]

QY	121	YMDYWGQGLVTSS	135
Db	121	VFDYWGQGLVTSS	135

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US-08-477-728-19
US-08-477-728-19
Sequence 19, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-728-19

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Query Match 75.7%: Score 545; DA 1; Length 135;
Best Local Similarity 77.8%: Pred. No. 2e-47;
Matches 105; Conservative 7; Mismatches 23; Indels 0; Gaps 0

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Db 1 MGSWMIIEFLLSAGTAGVSHSVQVOLVOSGAEVKKRGSSVKKVSCASGCTTETSYRHHWRQAP 60
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::

QY 61 GGGLEMIICVINYDNTNYYNOKFKGKATMYTKRSTSTAYMELSSLRSEPTAYYYCARAAM 120
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Db 61 GGGLEMIICVINYDNTNYYNOKFKGKATMYTKRSTSTAYMELSSLRSEPTAYYYCARAAM 120
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::

QY 121 YMDYWGQGTLEVYSS 135
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::

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Db          121.FDYWGQCTLVTVSS 135

RESULT      5
US-08-474-040-19
Sequence 19, Application US/08474040
Patent No. 5693761
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-474-040-19

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Query Match          75.7%  Score 545; DB 1; Length 135;
Best Local Similarity 77.8%  Pred. No. 2e-47;
Matches 105; Conservative 7; Mismatches 23; Indels 0; Gaps 0;

OY      1  MGNMCIFFLVTTATGVSQVQVLVDSGAEVKKPKGSSVKVYSCAGYTFITDVAIQWVROAP 60
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Db      1  MGNWSMIFLELTSGTGVHSQVQVLVDSGAEVKKPKGSSVKVYSCAGYTFITSRHWRQAP 60

OY      61  GGGLEWIMIVINYYNTYNTVNNOKFKKATPTVKKSTSTAYMELSSLRSEPTAYYYCARAAW 120
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      61  GGGLEWIMIGIYNPSTGYETNCKFKRATITADESINTATAMELSSLRSEPTAYYYCARGGG 120

OY      121  YMDTWGQGLTVTVSS 135
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

```

Db 121 VFDYWGQGLTVTVSS 135

RESULT 6

US-08-487-200-19

Sequence 19, Application US/08487200
Patent No. 5693762

GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.

APPLICANT: CO, Man Sung

APPLICANT: SCHNEIDER, William P.

APPLICANT: LANDOLFI, Nicholas F.

APPLICANT: COELINGH, Kathleen L.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESS: Townsend and Townsend and Crew

STREET: 379 Lytton Avenue

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 7-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/634,278

FILING DATE: 19-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/290,975

FILING DATE: 28-DEC-1988

PRIOR APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 11823-002610

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 135 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-487-200-19

Query Match 75.7%; Score 545; DB 1; Length 135;

Best local similarity 77.8%; Pred. No. 2e-47;

Matches 105; Conservative 7; Mismatches 23; Indels 0; Gaps 0;

Db 121 VFDYWGQGLTVTVSS 135

QY 1 MGWNCIIFLVTATGVSQVQVSGAEVKKPGSSVSKASGYTFTDYAIGWRAP 60

Db 1 MGWNCIIFLVTATGVSQVQVSGAEVKKPGSSVSKASGYTFTDYAIGWRAP 60

QY 61 GGGLEWIGVINIYDNTNINOKFKGATVYDKSTSTAYMELSLRSEDYAVYCARAW 120

Db 61 GGGLEWIGVINIYDNTNINOKFKGATVYDKSTSTAYMELSLRSEDYAVYCARAW 120

QY 121 YMDYWGQGLTVTVSS 135

Db 121 YMDYWGQGLTVTVSS 135

Db 121 VFDYWGQGLTVTVSS 135

RESULT 7

US-08-303-569B-31

Sequence 31, Application US/08303569B
Patent No. 5859205

GENERAL INFORMATION:

APPLICANT: Adair, John R.

APPLICANT: Emstage, John S.

TITLE OF INVENTION: Humanised Antibodies

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESS: Woodcock Washburn Kurtz MacKiewicz & NO. 5859205-115

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 07-SEP-1994

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Trujillo, Doreen Yalko

REGISTRATION NUMBER: 35,719

REFERENCE/DOCKET NUMBER: CARP-0032

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 135 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-303-569B-31

Query Match 75.7%; Score 545; DB 2; Length 135;

Best local similarity 77.8%; Pred. No. 2e-47;

Matches 105; Conservative 7; Mismatches 23; Indels 0; Gaps 0;

Db 121 VFDYWGQGLTVTVSS 135

QY 1 MGWNCIIFLVTATGVSQVQVSGAEVKKPGSSVSKASGYTFTDYAIGWRAP 60

Db 1 MGWNCIIFLVTATGVSQVQVSGAEVKKPGSSVSKASGYTFTDYAIGWRAP 60

QY 61 GGGLEWIGVINIYDNTNINOKFKGATVYDKSTSTAYMELSLRSEDYAVYCARAW 120

Db 61 GGGLEWIGVINIYDNTNINOKFKGATVYDKSTSTAYMELSLRSEDYAVYCARAW 120

QY 121 YMDYWGQGLTVTVSS 135

Db 121 YMDYWGQGLTVTVSS 135

QY 121 YMDYWGQGLTVTVSS 135

Db 121 YMDYWGQGLTVTVSS 135

QY 121 YMDYWGQGLTVTVSS 135

Db 121 YMDYWGQGLTVTVSS 135

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QY 121 YMDYWGQGLTVTVSS 135

Db 121 YMDYWGQGLTVTVSS 135

QY 121 YMDYWGQGLTVTVSS 135

Db 121 YMDYWGQGLTVTVSS 135


```

1 ADDRESS: ALLEGRETTI & WINCOFF
2 STREET: 10 SOUTH WACKER DRIVE
3 CITY: CHICAGO
4 STATE: ILLINOIS
5 COUNTRY: U.S.A.
6 ZIP: 60606
7
8 COMPUTER READABLE FORM:
9 MEDIUM TYPE: Floppy disk
10 COMPUTER: IBM PC compatible
11 OPERATING SYSTEM: PC-DOS/MS-DOS
12 SOFTWARE: WORD PERFECT 5.1
13
14 CURRENT APPLICATION DATA:

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.23
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11611
FILING DATE: 30-NOV-1993
CLASSIFICATION: 1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,949
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.

TELEFAX: 202-
TELEEX: 248633

US-08-656-586-8

Query Match	73.5%	Score 529	DB 2:	Length 139
Best Local Similarity	74.1%	Pred. NO. 8.1e-46		
Matches 103; Conservative	10;	Mismatches 22;	Indels 4;	Gaps 1

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 DB 1 MGNMFWFLFLLSGTACVHSQVOLVSGAEVKKFGASVSKASGYTFTSYTHWVROAP 60
 QY 61 GGGLEMGVINYDNTNOKFKGKATMTVDKSTAYMELSLRSBDTAVYCARAAW 120
 DB 61 GGGLEMGVINYDNTNOKFKGKATMTVDKSTAYMELSLRSBDTAVYCARAAW 120
 QY 121 YMDYMGQGTLYTVSS 135
 DB 121 YMDYMGQGTLYTVSS 135

RESULT 15
 US-08-137-117D-102
 ; Sequence 102, Application US/08137117D
 ; Patent No. 5795965

GENERAL INFORMATION:
 APPLICANT: TSUCHIYA, Masayuki
 APPLICANT: SATO, Koh
 APPLICANT: BENDIG, Mary
 APPLICANT: JONES, Steven
 APPLICANT: SALDANHA, Jose
 TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
 TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
 NUMBER OF SEQUENCES: 158
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/137,117D
 FILING DATE: 20-DEC-1993
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/JP92/00544
 FILING DATE: 24-APR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 4-32084
 FILING DATE: 19-FEB-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 3-95476
 FILING DATE: 25-APR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: WEGNER, Harold C.
 REGISTRATION NUMBER: 25,258
 REFERENCE/DOCKET NUMBER: 53466/126/AOAK
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)672-5300
 TELEFAX: (202)672-5399
 TELEX: 904136
 INFORMATION FOR SEQ ID NO: 102:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 135 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-137-117D-102

Query Match 73.2%; Score 527; DB 1; Length 135;
 Best Local Similarity 75.6%; Pred. No. 1.2e-45;
 Matches 102; Conservative 8; Mismatches 25; Indels 0; Gaps 0;

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DB 1 MGNMFWFLFLLSGTACVHSQVOLVSGAEVKKFGASVSKASGYTFTSYTHWVROAP 60
 QY 61 GGGLEMGVINYDNTNOKFKGKATMTVDKSTAYMELSLRSBDTAVYCARAAW 120
 DB 61 GGGLEMGVINYDNTNOKFKGKATMTVDKSTAYMELSLRSBDTAVYCARAAW 120
 QY 121 YMDYMGQGTLYTVSS 135
 DB 121 YMDYMGQGTLYTVSS 135

Search completed: April 25, 2001, 09:37:09
 Job time: 27 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 29, 2001, 20:35:05 ; Search time 1433.84 Seconds

(without alignments)
1700.705 Million cell updates/sec

Title: US-09-249-011-7

Sequence: 1 atgagttaccagcgcccggt.....ggaccacagtggaataaaa 396

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 3078962356 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 4: gb_in1:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	336.2	84.9	406	94	U62050 Mus musculus
4	333.6	84.2	419	94	MM062050 Mus musculus
5	332	83.8	940	9	MM097570 Mus musculus
6	332	83.8	940	10	A44968 Sequence 24
7	301.4	76.1	401	94	MM4211EV X65774 M. musculus
8	298.2	75.3	402	94	M98042 Mouse Ig re
9	296	74.7	336	94	AF163745 Mus muscu
10	296	74.7	336	94	MD1GKVAR Z22063 M. domestica
11	296	74.7	339	94	AB028876 Mus muscu

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ORIGIN						
Query Match			85.9%	Score 340;	DB 94;	Length 462;
Best Local Similarity			91.2%;	Pred. No. 1,2e-101;		
Matches 361;	Conservative	0;	Mismatches	35;	Indels	0; Gaps 0;
QY	1	atggattcacagcgccaggcttctatatatgtcgtcgtcatatggatcttgacactgtggg	60			
Db	19	ATGAGTACAGGCCCCAGAGCTTATTATTTGCTGCGTATCGGTATCTGTGAACGGTGG	78			
QY	61	gaacattgtctggaacacagtcctccaagatcccttgtcgtctaagcttagagaagaagggcaact	120			
Db	79	GACATTGTGAGTGACACACTCCTCCATCCCTCCCTGCTGTGCAGCAGGAGAGAAGCTCACT	138			
QY	121	attagctgacaatcagctcagatcagtctgtctcaaacagtagaaaccgagaaaactacttggct	180			
Db	139	ATGAGCTGCAAAATCCAGTCAAGTCTGCTCAACAGTATTAACCCGAAGAACAATTCTTGGCT	198			
QY	181	tgttacacagcgaacacagcgcaagctcctctaaactgcatactgtcatctactgtgcatcactagg	240			

Db	259	GAATCTGGGGTCCCTGATTCGCTTCACAGGACAGTGGATCTGGGACAGATTTCACCTCTCAC	318
Qy	301	atcagcagctctgcagcgtctgaagacgttgccagtttattactgcacgcgaatcttataatctt	360
Db	319	ATCAGCAGTGTGCAGGCGTGAAGACCTGGCAGCTTATTACTGCACAGCAATCTTATAATCTT	378
Qy	361	tacacgttcgcagacagcgagggaccacaagtgtgaataaaa	396
Db	379	CGGACGTTCTGGTGGAGGCACCAAGCTGGAAATYCAA	414
RESULT	2		
LOCUS	AI3733		
DEFINITION	AI3733	480 bp	DNA
		variable region of a monoclonal antibody which cross reacts with 19	part 03-JAN-1994
ACCESSION	AI3733	known P.aeruginosa serotypes.	
VERSION	AI3733.1	GI:491741	
KEYWORDS			
SOURCE		synthetic construct.	
ORGANISM		synthetic construct	
REFERENCE		artificial sequence.	
AUTHORS		1 (bases 1 to 480)	
TITLE		Domdey,H., Marget,M. and von Specht,B.U.	
		Monoclonal antibodies to pseudomonas aeruginosa, their production	

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CDS

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BASE COUNT 115 a 117 c 136 g 112 t
ORIGIN

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Best Local Similarity 91.2%; Pred. No. 1.2e-101;

Matches 361; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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DB 37 ATGATTACAGAGCCAGGCTTATATGTGCTGCTGATGCTGATCTGGTACGTGGG 96
QY 61 gaattgtgtgacacagttccagatccctgtgctgtaagcttagagagagagccact 120
|||||
DB 97 GCAATGTGATGTACAGTCTCCATCCCTGCTGCTGTCAGCAGAGAGAAAGTCACT 156
QY 121 attagctgaatccagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 180
|||||
DB 157 ATGAGCTGCAATTCATTCAGAGTCTGCTCAACAGTATTAACCCGAAAGAACTTTGGCT 216
QY 181 tggatccagagaacacagagcagctctcctaaactgtctgtatctatctgtgacactag 240
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DB 217 TGGTACACAGAGAAACAGGCGCATCTCTTAACCTGGTGATCTACTGGGATCCACTAGG 276
QY 241 gaattgtgtgacacagttccagatccctgtgctgtaagcttagagagagagccact 300
|||||
DB 277 GAATCTGTGGGTCCTGTGATCGCTTCAACAGGCTGATCTGGGAGATTTCACTCACTCAC 336
QY 301 atcagcagctgtcagagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 360
|||||
DB 337 ATCAGCAGTGTGCGAGGTGAGAGACCTGACACTTATTAATCTGCAAGCAANTTTATATCTT 396
QY 361 tacagcttcgagacagagagacagtcagtcagtcagtcagtcagtcagtcagtcagtcag 396
|||||
DB 397 CGGACGTTGCGGTGGAGGACCAACGCTGAATCAAA 432

RESULT 3
LOCUS MMU62050 406 bp mRNA ROD 19-FEB-1997
DEFINITION Mus musculus polyreactive autoantibody, immunoglobulin light chain
kappa mRNA, partial cds.
ACCESSION U62050
VERSION U62050.1 GI:1438580
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 406)
AUTHORS Diaw,L., Magnac,C., Pritsch,O., Buckle,M., Alzari,P.M. and
Dighiero,G.
TITLE Structural and affinity studies of Igm polyreactive natural
autoantibodies
JOURNAL J Immunol. 158 (2), 968-976 (1997)
MEDLINE 97146071
REFERENCE 2 (bases 1 to 406)
AUTHORS Diaw,L., Magnac,C., Pritsch,O., Buckle,M., Alzari,P.M. and
Dighiero,G.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-1996) Laboratoire d'Immunohematologie et
d'Immunopathologie, Institut Pasteur, 28, rue du Dr. Roux, Paris
75724 Paris Cedex 15, France
FEATURES
source location/Qualifiers
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/strain="(CBA/NXBALR/C)F1"
/db_xref="taxon:10090"
/sex="male"
/note="hybridoma M25-9; 6-day-old spleen cells fused with
SP2/0 myeloma cells"
<1..>406
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/product="polyreactive autoantibody, immunoglobulin light
chain kappa"
/protein_id="AAB47613.1"
/db_xref="GI:1438581"
/translation="OVLILLVSGTCGDIYMSQSPSLAVSAGEKVTMSCKSSQSL
NSTRKNFLMYOQKPGOSPKLIYASREGVDPDRFTGSSGDTFLTISVQAE
DLAVYCKOSYNLRFGGSKLEIKRAAPVSIFFPCSE"

CDS

BASE COUNT 101 a 99 c 108 g 98 t
ORIGIN

Query Match 84.9%: Score 336.2; DB 94; Length 406;
Best Local Similarity 92.7%; Pred. No. 2.2e-100;

Matches 353; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 16 caagttctatattgtcgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgt 75
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DB 1 CAGGTTCTTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
QY 76 caagttccagatccctgtcgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgt 135
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DB 61 CAGTCTCATCTCTCCGCGCTGTGTACACAGAGAGAGAGTCACTATGAGCTGCAAAATTC 120
QY 136 agtcaagctgtcgtcaagaagtagaaccgagagagactactgtgtgtgtgtgtgtgtgtgt 195
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DB 121 AGTCAGAGTGTGCTCAACAGTAGAACCCGAAAGAACTTGTGCTGTGTGTGTGTGTGTGTGT 180
QY 196 ccagggcagctctcctaaactgtatctatctatctatctatctatctatctatctatctatct 255
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DB 181 CCAGGCGAGTCTCTTAACCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 240
QY 256 gacgcttcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag 315
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DB 241 GATGCTTCACACAGCAGAGATCTGCGACAGATTTCACTCAACACAGCAGTGTGAGG 300
QY 316 gctgaagcgtgagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 375
|||||
DB 301 GCTGAAGACTGGCAGATTATTAATCTGCAAGCAATCTTATTAATCTGATACAGCTTGGAGGG 360
QY 376 ggagccaagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag 396
|||||
DB 361 GCGACCAAGCTGGAGATTA 381

RESULT 4
LOCUS MMU97570 419 bp mRNA ROD 11-JUN-1997
DEFINITION Mus musculus immunoglobulin light chain variable region (IgK) mRNA,
partial cds.
ACCESSION U97570
VERSION U97570.1 GI:2183076
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 419)
AUTHORS Feijo,G.C.S., Sabbaga,J., Carneiro,C.R.W. and Brigido,M.M.
TITLE Variable region structure and Staphylococcal protein A binding
specificity of a mouse anti-laminin receptor monoclonal Igm
JOURNAL Immunology (1997) In press
MEDLINE 97146071
REFERENCE 2 (bases 1 to 419)
AUTHORS Brigido,M.M.
TITLE Direct Submission
JOURNAL Submitted (15-APR-1997) Biologia Celular, Universidade de Brasilia,

FEATURES
source
Campus Universitario, Asa Norte, Brasília, DF 70910-900, Brazil
Location/Qualifiers
1. .419
/organism="Mus musculus"
/strain="Balb/c"
/db_xref="taxon:10090"
/cell_line="1H12"
/cell_type="hybridoma"
1. .>419
/gene="IgK"
21. .>419
/gene="IgK"
/note="rearranged Vκ8 to Jκ1 region"
/codon_start=1
/product="Immunoglobulin light chain variable region"
/protein_id="AAB60862.1"
/db_xref="GI:2183077"
/translation="MDSQAOVILLILLVNSCTGDIWVSQSPSSIAVSGAEKVTMSCK
SSQSLKSTRNVLAMTQAKPGOSPKLITVASTRESGVDPRTGSGSGDTFLTILIS
SVQAEIDLAIYCKQSYNLRTEGGPKLEIKR"
BASE COUNT 105 a 101 c 115 g 98 t
ORIGIN

Query Match 84.2%; Score 333.6; DB 94; Length 419;
Best Local Similarity 90.2%; Pred. No. 1.6e-99;
Matches 357; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1 atgagatcacagggccaggcttctatatctgctgctctatggtatctggaacctgtgg 60
DB 21 ATGAGATTCAAGGCCCGAGGCTCTTATATTGCTGCTGCTATGGGTATGCTGTGG 80
QY 61 gacatgtgctgacacagctctccagatcccttgctgtaagcttaagagagagggccact 120
DB 81 GACATTGTGATGTCACAGTCTCCATCTCCCTGGCTGTGTGTCAGCAGAGAGAGTCACT 140
QY 121 attagctgcaaatccacagctcagagctgtctcaacagtagaaccggagagaactactgtgct 180
DB 141 ATGAGCTGCAAGTCCAGTCAAGTCTGCTCAAAAGTAGAACCAGAGAAATTACTGGCT 200
QY 181 tggtagcaacagaacccaaggagcctcctaaactgtctatctactcgggcatccactaag 240
DB 201 TGGTACACACAGAACCAAGGCGAGTCTCCAAACTGCTATCTACGTGGCATCCATAAG 260
QY 241 gaatcgggggtccctatcgctcagtggaagtgaatcttggaacagatcactccacc 300
DB 261 GAATCTGGGGTCCCTGATGCTTCACAGGACAGTGGATCTGGACATTTCACTCTCACC 320
QY 301 atcagcagctcgaagcgtgaagacgttgcagttattactgcaagcaatctataactt 360
DB 321 ATCAGCAGTGTGCGAGCTGAAGACCTGGCAATTATTACTGCAAGCAATCTTATATCTT 380
QY 361 tacagcttgacacagggagccaaagtgtgaaataaaa 396
DB 381 CGAGCTTGGTGAGGCCCCCAAGCTGGAATCAAA 416

RESULT 5
LOCUS A44968 940 bp DNA PAT 07-MAR-1997
DEFINITION Sequence 24 from Patent W09515382.
ACCESSION A44968
VERSION A44968.1 GI:2299554
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE
AUTHORS 1 (bases 1 to 940)
Rose,M.S., Boot,C., Copley,C.G., Paterson,D.S., Hall,S.M.,
Wright,A.F., and Blakey,D.C.
TITLE BINDING STRUCTURES DIRECTED AGAINST THE CA55.1 ANTIGEN
JOURNAL Patent: WO 9515382-A 24 08-JUN-1995;
ZENECA LTD (GB)

COMMENT Other publication GB 2297751 960814
Other publication CA 2174972 950608
Other publication CA 9409266 950605
Other publication AU 1113095 950619.
Location/Qualifiers
1. .940
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 241 a 266 c 213 g 220 t
ORIGIN

Query Match 83.8%; Score 332; DB 9; Length 940;
Best Local Similarity 89.9%; Pred. No. 5.6e-99;
Matches 356; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 atgagatcacagggccaggcttctatatctgctgctctatggtatctggaacctgtgg 60
DB 10 ATGAGATTCAAGGCCCGAGGCTCTTATATTGCTGCTGCTATGGGTATCTGAACCTGTGG 69
QY 61 gacatgtgctgacacagctctccagatcccttgctgtaagcttaagagagagggccact 120
DB 70 GACATTGTGATGTCACAGTCTCCATCTCCCTGGCTGTGTGTCAGCAGAGAGAGTCACT 129
QY 121 attagctgcaaatccacagctcagagctgtctcaacagtagaaccggagagaactactgtgct 180
DB 130 ATGAGCTGCAAAATCCAGTCAAGTCTCTCAACAGTAGAACCAGAAAGAACTACTGGCT 189
QY 181 tggtagcaacagaacccaaggagcctcctaaactgtctatctactcgggcatccactaag 240
DB 190 TGGTACACACAGAACCAAGGCGAGTCTCTTAACTGCTATCTATTGGCATCCATAAG 249
QY 241 gaatcgggggtccctatcgctcagtggaagtgaatcttggaacagatcactccacc 300
DB 250 ACATCTGGGGTCCCTGATGCTTCACAGGACAGTGGATCTGGACATTTCACTCTCACC 309
QY 301 atcagcagctcgaagcgtgaagacgttgcagttattactgcaagcaatctataactt 360
DB 310 ATCAGCAGTGTGCGAGCTGAAGACCTGGCAATTATTACTGCAAGCAATCTTATCTTT 369
QY 361 tacagcttgacacagggagccaaagtgtgaaataaaa 396
DB 370 CGAGCTTGGTGAGGCCCCCAAGCTGGAATCAAA 405

RESULT 6
LOCUS I64459 940 bp DNA PAT 07-OCT-1997
DEFINITION Sequence 24 from patent US 5665357.
ACCESSION I64459
VERSION I64459.1 GI:2481353
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 940)
Rose,M.Samuel, Boot,C., Copley,C.Graham, Paterson,D.Stephen,
Hall,S.Margaret, Wright,A.Firman and Blakey,D.Charles.
TITLE Antibodies recognizing tumor associated antigen CA 55.1
JOURNAL Patent: US 5665357-A 24 09-SEP-1997;
FEATURES Location/Qualifiers
1. .940
/organism="unknown"
BASE COUNT 241 a 266 c 213 g 220 t
ORIGIN

Query Match 83.8%; Score 332; DB 10; Length 940;
Best Local Similarity 89.9%; Pred. No. 5.6e-99;
Matches 356; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 atgagatcacagggccaggcttctatatctgctgctctatggtatctggaacctgtgg 60
DB 11 ATGAGATTCAAGGCCCGAGGCTCTTATATTGCTGCTGCTATGGGTATCTGAACCTGTGG 69

Db	20	ATGATGTCACAGGGCCAGGTTCTTATATTGCTGCTGATGGGATCTGGAACTGTGGG	69
Oy	61	gacatctgtctctgacacagctctccagattccctgtgtglaagcttagagagagagccact	120
Db	70	GACATTGTGATGTACAGATCTCCATCCCTCCCTGGCTGTGCAGACGAGAGAAAGGTACC	129
Oy	121	atttgctgcgaattccagtcagagtcgtctctcaacagctgaacccgagagaaactcttgct	180
Db	130	ATGAGCTGCAATCAATCACTGATCAGTCAAGTCTCTCTCAACAGTGAAGAACCCGAAAGAACTACTTGCTT	189
Oy	181	tgtgtaccagacgaagaaccagggcagccctccctaactgtgtgtactgtactgtggatccacagg	240
Db	190	TGTGTACCGACGAGAACCCAGGSCAATCTCTTAATGCTGTGATCTATTGGCATCCACTAGG	249
Oy	241	gaatctggaggtccctctgatacgtcttagtctgagctgagatctggagacagattcactctcac	300
Db	250	ACATCTGGGGTCCCTGATCCGCTTCACAGGAGTGTGATCTGGAGACAGATTCCACTCTACC	309
Oy	301	atcagcagctctgcagagcttgaagacgttggcagttattactgtacacgcaattcttaactct	360
Db	310	ATCAGCAGTGTGCAGGCTGAGACCTGGCAATTTATTATCTGAACGCAATCTTATTACTCTT	369
Oy	361	tacacgttctgcagacagggagaccaaagtgtgaataaaa	396
Db	370	CGGACGTTTCGCTGAGGCGACCAACCTGGAATTCAAA	405

Db 3 ATGATTCACAGCGCCAGGTTCTTATGTATGTAAGTCTGCTATGGATGATCTGGTACTGTGGG 62

Qy 61 gacatctgctctgacacagctctccagatctccctgctctglaagcttagagagagagccact 120

Db 63 GACATTGTGATGTACAGTCTCCATCCCTCCCTAGCTGTGTCAGTTGGAGAAAGTTACT 122

Qy 121 attagctgcaaatccacgctcagctcagctctgctcaacagttagaacccgagagaactacttgct 180

Db 123 ATGACCTCCAGGTCAGTCAGCAGGCGCTTTTATATGTAGCATCAAAAGAACTACTTGCC 182

Qy 181 tggtaacagcagaaacccagggcagcctctcaacttgcttctactctgtaggataccatagg 240

Db 183 TGGTACACAGCGAACCACGGGCGAGTCTCTTAATCGCTGATTACTGGGATCCACATAGG 242

Qy 241 gaatctgggctccctgcatcgctctcagctgagctgagctctgagacagattcactctaac 300

Db 243 GAATCTGGGGTCCCTGATCGCTTCAACGCAAGTGGATCTGGGACAGATTCACCTCACC 302

Qy 301 atcagcagctctgcagagctgaagaagctggcagcttatattactgacagcaactctata---at 357

Db 303 ATCAGCACTGTGAAGGCTGAGAGACTGTGCAGTTATTACGTCCAGCATTTATTATAGCTT 362

Qy 358 cttaacagcttcgcgacagaggagccaagtgtaaatataa 396

Db 363 CCGTACACGTTTCGAGGGGGGACCAAGCTGGAATAATAAA 401

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RESULT 7
MMLA21LEV
LOCUS MMLA21LEV 401 bp DNA ROD 15-JUN-1993
DEFINITION M.musculus DNA for Ige antibody light chain (VJ).
ACCESSION X65774
VERSION X65774.1 GI:312076
KEYWORDS Ige antibody; J-segment; light chain; V-region.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 401)
Kofler,H., Schmegs,I., Geley,S., Helmsberg,A., Varga,J.M. and
Kofler,R.
Mechanism of allergic cross-reactions--III. cDNA cloning and
variable-region sequence analysis of two Ige antibodies specific
for trinitrophenyl
Mol. Immunol. 29 (2), 161-166 (1992)
92178225

JOURNAL
MEDLINE
FEATURES
SOURCE

Location/Qualifiers
1..401
/organism="Mus musculus"
/db_xref="taxon:10090"
/cell_line="10ELa2 (ATCC-TIB142)"
3..>401
/codon_start=1
/product="Ige antibody light chain (VJ)"
/protein_id="CAA6558.1"
/db_xref="GI:312077"
/translacion="MDSQAQVLMILLMWSCGCDIVMSQSPSSLASVGEKVTMSCK
SSGSLIASNKNYLAWORRPGQSPKLLIYMASTRRESGVDRFTGSGGDFLITLTSK
SVKRAEDLAVVYCOHYHSSPYFGGFKLEIK"
3..>401
/product="Ige antibody light chain (VJ)"
3..62
365..>401
BASE COUNT 100 a 91 c 105 g 105 t
ORIGIN

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RESULT      8
MUSICKALA
LOCUS      MUSICKALA      402 bp      mRNA      ROD      14-JUL-1993
DEFINITION Mouse Ig rearranged K-chain mRNA V-region, 5' end.
ACCESSION  M98042
VERSION    M98042.1 GI:196749
KEYWORDS   V-region; hepatitis; immunoglobulin light chain; processed gene.
SOURCE     Mus musculus (strain BALB/c, sub-species domesticus) spleen cDNA to
           mRNA.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 402)
AUTHORS   Hong,H.J., Kim,A.K., Ryu,C.J., Park,S.S., Chung,H.K., Kwon,K.S.,
            Kim,K.U., Kim,J., and Han,M.
TITLE     Cloning and characterization of cDNA's coding for heavy and light
            chains of a monoclonal antibody specific for pre-S2 antigen of
            hepatitis B virus
            Gene 121, 331-335 (1992)
JOURNAL   93077049
MEDLINE
FEATURES
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            1. 402
                location=Qualifiers
                /organism="Mus musculus"
                /strain="BALB/C"
                /sub_species="domesticus"
                /db_xref="taxon:10090"
                /cell_line="H8"
                /cell_type="hybridoma"
                /tissue_type="spleen"
                /map="Chromosome 6"
                1. 60
                1. 402
                1. partial
                /codon_start=1
                /function="Specific for pre-S2 antigen of hepatitis B
                virus"
                /product="immunoglobulin kappa-chain"
                /protein_id="AAA38777.1"
sig-peptide
CDS

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	Query Match	76.1%	Score 301.4	DB 94	Length 401
	Best Local Similarity	86.5%	Pred. No. 7.6e-89		
	Matches 345	Conservative 0	Mismatches 51	Indels 3	Gaps 1
OY	1 atgagttcaagagccaggcttctatattctgctgcgtacatggtatctgcgaacctgtggg				60

mat_peptide 102 a 93 c 100 g 107 t

BASE COUNT 102 a 93 c 100 g 107 t

ORIGIN

Query Match 75.3%; Score 298.2; DB 94; Length 402;
 Best Local Similarity 86.0%; Pred. No. 8.7e-88;
 Matches 343; Conservative 0; Mismatches 53; Indels 3; Gaps 1;

OY 1 atgagctacagagccaggtcttattctgtctgtcattgggtatctggcactgtgg 60
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 1 ATGGATTACAGAGCCAGGTTCTTATGTTACTGCTGATGGTATCTGATCCTGTGG 60
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

OY 61 gacattgtctgtacagatctccagattccctgctgtgtaagcttagagagagggccact 120
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 61 GACATTGTGATGTACAGTCTTCATCTCCCTAGCTGTGTAGTTGGAGAGAGTTACT 120
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

OY 121 attagctcaaatccagtcagagtcgtctcaacagtagaacccgagagaactactgtgct 180
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 121 ATGACTTCGAATCCAGTCAGAGCCTTTATATATAGTACATTCAAAAGAACTACTGGCC 180
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

OY 121 atgactcgaatccagtcagagtcgtctcaacagtagaacccgagagaactactgtgct 180
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 121 ATGACTTCGAATCCAGTCAGAGCCTTTATATATAGTACATTCAAAAGAACTACTGGCC 180
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OY 181 tggtaaccagagaacccagagccctctaaactgtctactatctgggcatccactagg 240
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 Db 181 TGGTACAGCAGAAACAGGCGAGTCTCTAAACTGTGATTTACTGGCATCCACTAGG 240
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OY 241 gaattcgggtccctcgtcagtcagtcagtgagatctggagacagattcactctacc 300
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 Db 241 GAATCTGGGGTCCCTGATCGCTTCACAGCAGTGTGATGTGAGATTTCACTCTCACC 300
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

OY 301 atcagcagctcgcagcgcgaagcgtgacgttatactgaacgaactctata---at 357
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 301 ATCAGCATGTGTAAGCGCTGAAGACCTGGCAGTTTATTTACTGTCAGCATATTATATACAT 360
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OY 358 cttaacacgttcgcagagaggggacgaagltggaataaaa 396
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 Db 361 CCGTCCACGTTCCGAGGGGAGGACCTCACTCGAATAATAAA 399
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RESULT 9
 AF163745 336 bp mRNA ROD 04-AUG-1999
 LOCUS Mus musculus mab 27.4.1 immunoglobulin light chain variable region
 DEFINITION AF163745
 mRNA, partial cds.
 ACCESSION AF163745
 VERSION AF163745.1 GI:5690296
 KEYWORDS house mouse.
 SOURCE Mus musculus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 336)
 AUTHORS Mertens,N.M., Galvin,J.E., Adderson,E.E. and Cunningham,M.W.
 TITLE Molecular Analysis of Crossreactive Anti-Myosin/Anti-Streptococcal
 Mouse Monoclonal Antibodies
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 336)
 AUTHORS Mertens,N.M. and Cunningham,M.W.
 TITLE Direct Submission
 JOURNAL Submitted (03-JUN-1999) Microbiology and Immunology, Oklahoma
 University Health Sciences Center, 940 St. Young Blvd, Oklahoma
 City, OK 73190, USA
 FEATURES
 source location/Qualifiers
 1. 336
 /organism="Mus musculus"
 /strain="BALB/c"
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 /product="immunoglobulin light chain variable region"
 /protein_id="A047024.1"
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 /translation="DIVSOSPSSLAWSAGEKWTMSCKSSSLNSRTRKNYLAWYOO
 KPGSGPKLIYMASTRSGVDPDRFTSGSGSDFTLTISVQAEMLAVYYCKOSINLYT
 FGGSTKLEIK"
 BASE COUNT 91 a 83 c 86 g 76 t

ORIGIN

Query Match 74.7%; Score 296; DB 94; Length 336;
 Best Local Similarity 92.6%; Pred. No. 4.7e-87;
 Matches 311; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

OY 61 gacattgtctgtacagatctccagattccctgctgtgtaagcttagagagagggccact 120
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 1 GACATTGTGATGTACAGTCTTCATCTCCCTGCTGTGTCAGAGAGAGAGAGTCACT 60
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

OY 121 attagctcgaatccagtcagagtcgtctcaacagtagaacccgagagaactactgtgct 180
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 61 ATGAGCTGCAATATCCAGTCAGAGTCTCTCAACAGTGAACCCGAAAGAACTACTGGCT 120
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

OY 181 tggtaaccagagaacccagagccctctaaactgtctactatctgggcatccactagg 240
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 121 TGGTACAGCAGAAACAGGCGAGTCTCTAAACTGTGATTTACTGGCATCCACTAGG 180
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

OY 241 gaattcgggtccctcgtcagtcagtcagtgagatctggagacagattcactctacc 300
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 181 GAATCTGGGGTCCCTGATCGCTTCACAGCAGTGTGATGTGAGATTTCACTCTCACC 240
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OY 301 atcagcagctcgcagcgcgaagcgtgacgttatactgaacgaactctataactct 360
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 Db 241 ATCAGCATGTGTCAGGCTGAAGACCTGGCAGTTTATTTACTGTCAGCATATTATATCTG 300
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OY 361 tacacgttcgcagagagggagaccaggtggaataaaa 396
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 Db 301 TACAGTTTCGGAGGGGAGGACCAAGCTGGAATAATAAA 336
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RESULT 10
 MDIGKVAR 336 bp mRNA ROD 05-NOV-1994
 LOCUS M.domesticus Iqg variable region.
 DEFINITION 222063.1 GI:297629
 ACCESSION 222063.1
 VERSION 222063.1 GI:297629
 KEYWORDS anti-DNA antibody; Iqg gene; Iqg variable region; immunoglobulin.
 SOURCE western European house mouse.
 ORGANISM Mus musculus domesticus
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 336)
 AUTHORS Tillman,D.M., Jou,N.T., Hill,R.J. and Marion,T.N.
 TITLE Both Iqg and Iqg anti-DNA antibodies are the products of clonally
 selective B cell stimulation in (NZB x NZM)F1 mice
 JOURNAL J. Exp. Med. 176 (3), 761-779 (1992)
 MEDLINE 92381444
 REFERENCE 2 (bases 1 to 336)
 AUTHORS Marion,T.N.
 TITLE Direct Submission
 JOURNAL Submitted (23-MAR-1993) Tony N. Marion, Microbiology and
 Immunology, University of Tennessee, Memphis, 858 Madison Avenue,
 Memphis, TN, 38163, USA
 FEATURES
 source location/Qualifiers
 1. 336
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 /dev_stage="somatic variant"
 /tissue_type="spleen"
 /cell_type="hybridoma"
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 1. 336
 /gene="Iqg"
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 /function="kappa light chain variable region for anti-DNA
 antibody; Vx8 family"

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/codon_start=1
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KPGSPKLIYMASTRSGVDPDRFTSGSGSDFTLTSSVOAEDLAYVYCKOSYNLYT
FGGSKLEIK"

BASE COUNT      91 a      83 c      86 g      76 t
ORIGIN

Query Match      74.7%; Score 296; DB 94; Length 336;
Best Local Similarity 92.6%; Pred. No. 4.7e-87;
Matches 311; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

OY 61 gacattgctgacacagctccagatccctgctgtgtaagcttagagagagccact 120
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 1 GACATTGTGATGTCACAGCTCCATCCTCCCTGCTGTCTCAGCAGAGAGAGTCACT 60
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

OY 121 attagctgaatccagtcagagctgtctcacaagtagaaccggagagacttgct 180
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 61 ATGACTGCAATCCAGTCAGAGTCTCTCAACAGTAGAACCCGAAAGACTTGGCT 120
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

OY 181 tggtaaccagcagaaccaggcagcctcctaaactgctgactatctagggcactag 240
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 121 TGGTACGACGAAACAGGCGCATCTCTTAAGTGTGATCTACTGGGCATCCACTAG 180
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

OY 241 gaattggggtccctgactgcttcagtgagtgatctggagacatttcactcacc 300
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 181 GAATCTGGGGTCCCTGATGCTTTCACAGCGCATGTGGGACAGATTTCACCTCCACC 240
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

OY 301 atccagcagctcgcagcgtgaagcgtgcaagtattactgacccaattctatactt 360
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 241 ATCAGCAGTGTCTCAGGCTGAAGACCTGGCAGTTTATATCTGACAGCAATCTTATATCTG 300
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

OY 361 tacacgttcgacagcaggaccaaaggtggaataaaa 396
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 301 TACAGCTTCGAGGGGGGACCAAGCTGGAAATATAA 336
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

RESULT 11
AB028876      339 bp      mRNA      ROD      07-DEC-1999
LOCUS      Mus musculus mRNA for 5.2 Igg light chain (variable region),
DEFINITION      partial cds.
ACCESSION      AB028876
VERSION      AB028876.1 GI:5103290
KEYWORDS      5.2 Igg light chain variable region.
SOURCE      Mus musculus cell_line:hybridoma 5.2 cDNA to mRNA.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Yoshida,S., Matsuo,K., Luo,E., Iwai,K., Arai,M., Sinden,R.E. and
Ishii,A.
TITLE      A single-chain antibody fragment specific for the Plasmodium
berghel ookinete protein Pbs21 confers transmission blockade in the
mosquito midgut
Mol. Biochem. Parasitol. 104 (2), 195-204 (1999)
20058748
2 (bases 1 to 339)
Yoshida,S.
DIRECT SUBMISSION
Submitted (11-JUN-1999) to the DDBJ/EMBL/GenBank databases. Shigeto
Yoshida, Jichi Medical School, Department of Medical Zoology;
Yakushiji 3311-1, Minamikawachimachi, Tochigi 329-0498, Japan
(E-mail:shigeto@jichi.ac.jp, Tel:81-285-58-7339,
Fax:81-285-44-6489)
FEATURES
Source      1..339
            Location/Qualifiers
            /organism="Mus musculus"
            /db_xref="taxon:10090"
            /cell_line="hybridoma 5.2"
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gene      1..339
           /gene="5.2 VL"
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CDS      /gene="5.2 VL"
           /note="light chain variable region of 5.2 monoclonal
           antibody"
           /codon_start=1
           /product="5.2 Igg light chain"
           /protein_id="AA78904.1"
           /db_xref="GI:5103291"
           /translation="DIVMSQSPSSLVAGSKVYMSCKSSQSLNSRTRKLYLWYQ
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           FGGSKLEIK"

BASE COUNT      92 a      84 c      87 g      76 t
ORIGIN

Query Match      74.7%; Score 296; DB 94; Length 339;
Best Local Similarity 92.6%; Pred. No. 4.7e-87;
Matches 311; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

OY 61 gacattgctgacacagctccagatccctgctgtgtaagcttagagagagccact 120
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 1 GACATTGTGATGTCACAGCTCCATCCTCCCTGCTGTCTCAGCAGAGAGAGTCACT 60
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

OY 121 attagctgaatccagtcagagctgtctcacaagtagaaccggagagacttgct 180
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 61 ATGACTGCAATCCAGTCAGAGTCTCTCAACAGTAGAACCCGAAAGACTTGGCT 120
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

OY 181 tggtaaccagcagaaccaggcagcctcctaaactgctgactatctagggcactag 240
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 121 TGGTACGACGAAACAGGCGCATCTCTTAAGTGTGATCTACTGGGCATCCACTAG 180
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OY 241 gaattggggtccctgactgcttcagtgagtgatctggagacatttcactcacc 300
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 181 GAATCTGGGGTCCCTGATGCTTTCACAGCGCATGTGGGACAGATTTCACCTCCACC 240
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

OY 301 atccagcagctcgcagcgtgaagcgtgcaagtattactgacccaattctatactt 360
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 241 ATCAGCAGTGTCTCAGGCTGAAGACCTGGCAGTTTATATCTGACAGCAATCTTATATCTG 300
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

OY 361 tacacgttcgacagcaggaccaaaggtggaataaaa 396
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 301 TACAGCTTCGAGGGGGGACCAAGCTGGAAATATAA 336
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

RESULT 12
S81289      408 bp      mRNA      ROD      23-MAY-1996
LOCUS      Igm kappa chain variable region [CDR1 to CDR3 region] [rats, LEW,
DEFINITION      HAR-1 hybridoma cells, mRNA Partial, 408 nt].
ACCESSION      S81289
VERSION      S81289.1 GI:1326409
KEYWORDS
SOURCE      Rattus sp. LEW HAR-1 hybridoma cells.
ORGANISM      Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
Borle,D.C., Cramer,D.V., Shirvan,H., Wu,G.D., Rodriguez,O.,
Chapman,F.A. and Makowka,L.
Genetic control of the humoral immune response to xenografts. II.
Monoclonal antibodies that cause rejection of heart xenografts are
encoded by germline immunoglobulin genes
Transplantation 60 (12), 1504-1510 (1995)
96125839
JOURNAL      GenBank staff at the National Library of Medicine created this
MEDLINE      entry [NCBI gibs9 176405] from the original journal article.
REMARK      This sequence comes from Fig. 4.
            Location/Qualifiers
            1..408
            /organism="Rattus sp."
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/gene="igm kappa chain variable region"
/notice="hamster heart xenograft rejection-associated; ;
This sequence comes from Fig. 4"
/codon_start=1
/product="igm kappa chain variable region"
/protein_id="AAB35891.1"
/db_xref="gi:1326410"
/translation="MESOTOWLSLILWSTGCGDIYMTQPPSOAVSAGEKVMTSK
SSGLILNENKNKLYLAKCPQSPFLIYIWAATRESGVDPDRITGSGIDFLITLIS
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BASE COUNT
106 a 100 c 108 g 94 t
ORIGIN

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Query Match	74.5%	Score 295.2	DB 95	length 408
Best Local Similarity	84.1%	Pred. No. 8.6e-87		
Matches 333	Conservative 0	Mismatches 63	Indels 0	Gaps 0

Oy	1	atggtttcaagagcccaagtccttatattgtcgcgcgaatgtaatcggcaaccgttgg	60
Db	7	atggatatacacacacacaggtctctcatgtgccgtgctcttggtatcttgtaacctgtggg	66
Oy	61	gacattgtctgacacagtcctcaaatctccatgctcgtgcgtgtaagccttagagaagagggccaat	120
Db	67	gacatttgatgatgaccacacagctctcatctccacgctgtgtgacgacggagaaaggttacct	126
Oy	121	attagctgcacaaatccagtcagatcctgtctcaacagtagaacccgaagaaactattgct	180
Db	127	atgacctgcacaaatccacgacagctgtttttatcattatgaaacaaamaaacacttctggcc	186
Oy	181	tgtgtccagagcaaaaacagagggcagcctctcttaacgtgcgaatcttaattggcaatccacatgg	240
Db	187	tgtgtccacgacaaacacacagggcagctctcttaacgtgcgaatcttaattggcaatccacatgg	246
Oy	241	gaattctgggtccctcgaatcgcgtcttcagttgacgttgatcttgagacgaatctcaactccacc	300
Db	247	gaattctgggggtccctcgaatcgcgtcttcatataggacatgatctgggacagatttctactcttgacc	306
Oy	301	atccagcagctctgcagagctgaaagcgttgycagttatctactgcacgcaatctataatcct	360
Db	307	atccagcagctctgcagagcagaagacctgctgtttttactgcccacacacttactatataacttgg	366
Oy	361	tacacgtctgcagacagaggaacagattggaataataaa	396
Db	367	ttaacgcttttggaagctgggacacacagcttggaactggaaa	402

RESULT	13
MUSIGKV130	
LOCUS	MUSIGKV130
DEFINITION	Mus musculus Ig rearrange kappa-chain gene V19-J1 region.
ACCESSION	L16819
VERSION	L16819.1
KEYWORDS	GI:293622
SOURCE	V-region; complementarity determining region; immunoglobulin light chain; kappa-immunoglobulin; processed gene.
ORGANISM	Mus musculus (strain NZB/W F1) mRNA.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 339)
TITLE	Lustgarten,D.L., Kavalier,J., Gerhard,W. and Scharff,M.D. The response to a foreign antigen in the autoimmune NZB/W F1 murine strain Unpublished (1993) Location/Oallifiers 1..339 "/organism="Mus musculus"
JOURNAL	
FEATURES	
source	+

	/strain="NZ/CP01.1"	
	/db_xref="taxon:10090"	
	/cell_line="BWS-130"	
	/cell_type="hybridoma"	
V_region	1..285	
	/gene="Igk-V19"	
	/standard_name="V19"	
gene	1..324	
	/gene="Igk-V19"	
	70..102	
misc_feature	/gene="Igk-V19"	
	/standard_name="CDR1"	
	148..168	
misc_feature	/gene="Igk-V19"	
	/standard_name="CDR2"	
	265..291	
misc_feature	/gene="Igk-V19"	
	/standard_name="CDR3"	
	286..324	
J_segment	/gene="Igk-V19"	
	/standard_name="J1"	
BASE COUNT	89 a 85 c 88 g 76 t 1 others	
ORIGIN		

Query Match	74.5%	Score 295	DB 94	Length 339
Best Local Similarity	92.3%	Pred. No. 1e-86		
Matches 310	Conservative 0	Mismatches 26	Indels 0	Gaps 0

Oy	61	gaattgagctgacacacatctcccaattccctggctgtgaagtttagggagaaggccact	120
Db	1	GACATTGTGATGTCACAGTCTTCANCTCCCTGGCTGTCTCAGCAGGAGAGGGTCACT	60
Oy	121	attaagctgcaaaatccagttcagaagatctgtctcaacagtagaaccggagagaactacttgct	180
Db	61	ATGACCTGCAATCCAGATCAGATGCTGTGCTCAACACTAGAACCCGGAAGAACTACTTGGGT	120
Oy	181	tgtatcccgacgaaaacccagggagcagctccctaaacgctcatctactatggatcccaactagg	240
Db	121	TGGTACCGACGAACACCAAGGCGAGTCTCTTAACATGCTGATTTACTGGGCATCCACTAGG	180
Oy	241	gaattgsggtccctgatcogcttcactagttgacgttgatctggagacagatltcactctacc	300
Db	181	GAATGTGGGGTCCCTGATTCGCTTTCACAGGACAGTGATCTGGGACAGATTCACCTTCACC	240
Oy	301	atccagcagcttcgacgctcgaaagaagctggcagtttaactgaacgcaatcttaaatct	360
Db	241	ATTCACAGTGTGCACAGCTGGAACACTCTGGCAGTTTATTACTGCAACACANTCTATATCTT	300
Oy	361	tacacgttcgcgaagagggaaccaagtgtagaataaataa	396
Db	301	TACACGTTTCGAGGGGNGAGCAACGCTGGGAAAAAATAA	336

RESULT 14			
LOCUS	MDIGGVAI	336 bp	05-NOV-1994
DEFINITION	M.domesticus IgG variable region.		
ACCESSION	222039		
VERSION	222039.1		
KEYWORDS	anti-IgM antibody; IgG gene; IgG variable region; immunoglobulin.		
SOURCE	western European house mouse.		
ORGANISM	Mus musculus domesticus		
	Eumaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;		
	Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 336)		
AUTHORS	Tillman,D.M., Jou,N.T., Hill,R.J. and Marlon,T.N.		
TITLE	Both IgM and IgG anti-IgM antibodies are the products of clonally		
	selective B cell stimulation in (NZB x NZM)F1 mice		
JOURNAL	J. Exp. Med.	176 (3), 761-779	(1992)
MEDLINE	9238144		
REFERENCE	2 (bases 1 to 336)		
AUTHORS	Marlon,T.N.		

TITLE Direct Submission
JOURNAL Submitted (23-MAR-1993) Tony N. Marion, Microbiology and Immunology, University of Tennessee, Memphis, 858 Madison Avenue, Memphis, TN 38163, USA

FEATURES

Source

Location/Qualifiers
1. .336
/organism="Mus musculus domesticus"
/strain="(NZB x NZW)F1"
/isolate="mouse #163"
/db_xref="taxon:10092"
/chromosome="6"
/sex="Female"
/dev_stage="somatic variant"
/tissue_type="spleen"
/cell_type="hybridoma"
/cell_line="163.1"
1. .336
/gene="Igc"
/gene="Igc"
/gene="Igc"
/function="kappa light chain variable region for anti-DNA antibody; Vx8 family"
/note="163.1 is clonally related to the Igc hybridomas 163.14, 163.37, 163.64, 163.77, 163.106, 163.124, 163.132, and 163.133 in the 163-cl clone"
/codon_start=1
/product="immunoglobulin variable region"
/protein_id="CA80013.1"
/db_xref="GI:297577"
/translation="DIVMSQSPSLAVSAGEKYTMCKSSQSLNSRTRKNLYAYQO KPGSPRLIYMASTRSGVDPDFGTSGSGTDFTLTITSSVQADLAVYYCKQSYNYLT FGSGTKLEIK"

BASE COUNT 90 a 82 c 88 g 76 t
ORIGIN

Query Match 73.9%; Score 292.8; DB 94; Length 336;
Best Local Similarity 92.0%; Pred. No. 5.4e-86;
Matches 309; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

OY 61 gacatgtgctgacacagctccagatccctgctgtaagcttagagagagagccact 120
|||||
DB 1 GACATGTGTGATGTACAGTCTCCATCTCCCTGCTGTGTCAGAGAGAGAGTCACT 60
OY 121 attagctgcaaatcagtcagagctgctcaacagctagaaccgagagaaacttggct 180
|||||
DB 61 ATGAGCTGCAAAATCCAGTCAAGTCTCTCAACAGTAGAAACCCGAAAGAACTACTTGGCT 120
OY 181 tggtaaccagcaagaaccagagcagctcccttaactgctgactctactgagacactagg 240
|||||
DB 121 TGGTACCAAGCAAGAAACCAAGGCACTCTTAATGCTGATCTACTGGGCATCCAGTAGG 180
OY 241 gaactgggtgccctgtaactgctcagtgagctgagatctggagaaattcaactccacc 300
|||||
DB 181 GAATCTGGGGTCCCTGATGCTTCAACAGCGAGTGATCGGAGACAGATTTCACCTCACCC 240
OY 301 atcagcagctgcaagctggaagcgttgcaattactactcaacgcaacttataactct 360
|||||
DB 241 ATCAGCACTGTGACAGCGCTGAAGACCTGGCAGTTATTACTCAAGCAATTTATATCTG 300
OY 361 tacacgttcgacacagggagaccaggtggaataaaa 396
|||||
DB 301 TACACGTTTCGGGGGGGGGACCAAGCTGGAATATAAA 336

RESULT 15
LOCUS MDIGKVAU 336 bp mRNA
DEFINITION M.domesticus Igc variable region.
ACCESSION 222070
VERSION 222070.1 GI:297635
KEYWORDS anti-DNA antibody; Igc gene; Igc variable region; immunoglobulin.
SOURCE western European house mouse.

ORGANISM

Mus musculus domesticus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 336)
Tillman,D.M., Jou,N.T., Hill,R.J. and Marion,T.N.
Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell stimulation in (NZB x NZW)F1 mice
J. Exp. Med. 176 (3), 761-779 (1992)

JOURNAL

92381444

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

Location/Qualifiers
1. .336
/organism="Mus musculus domesticus"
/strain="(NZB x NZW)F1"
/isolate="mouse #165"
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/dev_stage="somatic variant"
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/cell_line="165.5"
1. .336
/gene="Igc"
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/gene="Igc"
/function="kappa light chain variable region"
/note="165.5 is clonally related to the Igc hybridomas 163.14, 163.37, 163.64, 163.77, 163.106, 163.124, 163.132, and 163.133 in the 163-cl clone"
/codon_start=1
/product="immunoglobulin variable region"
/protein_id="CA80044.1"
/db_xref="GI:297636"
/translation="DIVMSQSPSLAVSAGEKYTMCKSSQSLNSRTRKNLYAYQO KPGSPRLIYMASTRSGVDPDFGTSGSGTDFTLTITSSVQADLAVYYCKQSYNYLT FGSGTKLEIK"

BASE COUNT 91 a 83 c 86 g 76 t
ORIGIN

Query Match 73.9%; Score 292.8; DB 94; Length 336;
Best Local Similarity 92.0%; Pred. No. 5.4e-86;
Matches 309; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

OY 61 gacatgtgctgacacagctccagatccctgctgtaagcttagagagagagccact 120
|||||
DB 1 GACATGTGTGATGTACAGTCTCCATCTCCCTGCTGTGTCAGAGAGAGAGTCACT 60
OY 121 attagctgcaaatcagtcagagctgctcaacagctagaaccgagagaaacttggct 180
|||||
DB 61 ATGAGCTGCAAAATCCAGTCAAGTCTCTCAACAGTAGAAACCCGAAAGAACTACTTGGCT 120
OY 181 tggtaaccagcaagaaccagagcagctcccttaactgctgactctactgagacactagg 240
|||||
DB 121 TGGTACCAAGCAAGAAACCAAGGCACTCTTAATGCTGATCTACTGGGCATCCAGTAGG 180
OY 241 gaactgggtgccctgtaactgctcagtgagctgagatctggagaaattcaactccacc 300
|||||
DB 181 GAATCTGGGGTCCCTGATGCTTCAACAGCGAGTGATCGGAGACAGATTTCACCTCACCC 240
OY 301 atcagcagctgcaagctggaagcgttgcaattactactcaacgcaacttataactct 360
|||||
DB 241 ATCAGCACTGTGACAGCGCTGAAGACCTGGCAGTTATTACTCAAGCAATTTATATCTG 300
OY 361 tacacgttcgacacagggagaccaggtggaataaaa 396
|||||
DB 301 TACACGTTTCGGGGGGGGGACCAAGCTGGAATATAAA 336

Search completed: April 29, 2001, 20:35:07
Job time: 5614 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 29, 2001, 20:11:00 ; Search time 1635.84 seconds
(without alignments)
35.383 Million cell updates/sec

Title: US-09-249-011-7
Perfect score: 396
Sequence: 1 atgattcacagagccacagt.....ggaccaagtggaataaaa 396

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 segs, 73081774 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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101: em_esthum67:*
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105: em_esthum71:*
106: em_esthum72:*
107: em_esthum73:*
108: em_esthum74:*
109: em_esthum75:*
110: em_esthum76:*
111: em_esthum77:*
112: em_esthum78:*
113: em_esthum79:*
114: em_esthum80:*
115: em_esthum81:*
116: em_esthum82:*

```

117: gb_est48:*
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119: gb_est50:*
120: gb_est51:*
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122: gb_est53:*
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132: gb_est63:*
133: gb_est64:*
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141: gb_est72:*
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161: gb_est92:*
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176: gb_est107:*
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185: gb_est116:*
186: gb_est117:*
187: gb_est118:*
188: gb_est119:*
189: gb_est120:*

```

Result No.	Score	Match	Length	ID	Description
1	312	78.8	905	BF580037	BF580037 602095235
2	272.8	68.9	691	BF128999	BF128999 601811318
3	258.6	65.3	300	BG148633	BG148633 u085B09.Y
4	256	64.6	641	AW405821	AW405821 UI-HF-BL0
5	253.4	64.0	643	AW390292	AW390292 CM2-ST018
6	251	63.4	886	BF674779	BF674779 602137932
7	247.6	62.5	508	AW406572	AW406572 UI-HF-BL0
8	244	61.6	388	BF663188	BF663188 602144432
9	240.6	60.8	573	AW951579	AW951579 EST363649
10	231.4	58.4	887	BF128857	BF128857 601811013
11	229.6	57.0	401	BF128857	BF128857 601810838
12	228.4	57.7	533	AV685285	AV685285 AV685285
13	228.4	57.7	558	AW802126	AW802126 IL5-UM007
14	227.2	57.4	553	BF964753	BF964753 602267977
15	226.6	57.2	503	BF830413	BF830413 RCI-HT025
16	226.2	57.1	550	AW404610	AW404610 UI-HF-BL0
17	224.6	56.7	403	AV734428	AV734428 AV734428
18	224.6	56.7	630	AW406512	AW406512 UI-HF-BL0

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19 221.8 56.0 444 168 BF746228
20 221.8 56.0 444 168 BF746298
21 221.6 56.0 397 168 BF746298
22 220.8 55.8 328 114 AM406484
23 220.4 55.7 847 151 BF678476
24 219.8 55.5 655 31 AV702633
25 219.4 55.4 553 170 BF870122
26 217.8 55.0 363 156 AA300651
27 215.2 54.3 364 156 T27579
28 201.2 50.8 349 122 AM947280
29 200 50.5 459 114 AM383565
30 198.2 50.1 410 172 BG059215
31 194.2 49.0 333 115 AM407858
32 190.2 48.0 425 24 A1734035
33 190.2 48.0 442 7 AA405415
34 188.4 47.6 423 115 AM406796
35 187 47.2 594 165 BE309592
36 187 47.2 597 170 BF868788
37 185.2 46.8 480 170 BF877467
38 183.2 46.3 1153 151 BF663521
39 182.2 46.0 488 114 AM405725
40 181.8 45.9 445 114 AM405178
41 181.8 45.9 488 153 H25625
42 181 45.7 363 7 AA464313
43 180.6 45.6 454 115 AM406883
44 180.2 45.5 409 138 BE719012
45 179.8 45.4 504 114 AM405787

ALIGNMENTS

RESULT 1
LOCUS BF580037 905 bp mRNA
DEFINITION 602095235F1 NCT_CGAP_Co24 Mus musculus cDNA clone IMAGE:4209417 5',
mRNA sequence.
ACCESSION BF580037
VERSION BF580037.1 GI:11653749
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: L1AM9775 row: f column: 10
High quality sequence stop: 757.
Location/Qualifiers
1. 905
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4209417"
/lab_host="NCT_CGAP_Co24"
/note="Organ: colon: Vector: PCMV-SPOPT6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCT_CGAP Library."

FEATURES

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BASE COUNT

248 a 236 c 217 g 204 t

ORIGIN

Query Match

78.8%; Score 312.; DB 150; Length 905;

Best Local Similarity 91.7%; Pred. No. 2e-85;

Matches 363; Conservative 0; Mismatches 30; Indels 3; Gaps 3;

QY 1 atgattcacagagccaggttcattatattctgtctgtatggatctggcacttggg 60
DB 18 ATGATTACAGAGCCAGGTTCTTATA-TGCTGCTGTAAGGTATCTGCTGTGGG 76
QY 61 gacatttgcctgacagcagcttcagattcccttgcgtgtaagtaagagagagccact 120
DB 77 GACA-TGTGATGTCACAGCTCCATCCTCGCTGCTGTACAGAGAGAGAGATCCT 135
QY 121 attagctgcaaatccatctcagatctgtctcacaagtaaacccgagagacttggct 180
DB 136 ATGAACATGCAAAATCCAGATGCTCTCAACAGTGAATCCGAAAGAACTACTGGCT 195
QY 181 tggaccacagagaacacagagcagccctcctaactgtctgtacttacttggcattcagtag 240
DB 196 TGGTACACAGCAGAAACCA-GGCACTCTCTAACTGCTGATCTAGTGGCATCCACTAGG 254
QY 241 gaatctggggctccctgactcgtctcagtgagtgatcttggacaagattcactctacc 300
DB 255 GAATCTGGGCTCCCTGATCCTTCACAGCAGTGTGAGATGTCAGATTCACCTCACC 314
QY 301 atcagcagcttcgacagctgaagaagctggcagttattacttcagcagcatttataactt 360
DB 315 ATCAGCAGTGTGACAGGCTGAAGACCTGTATTATTCGAAGCAATCTTAACTT 374
QY 361 tacacgttcgacagagggacgaagtggaataana 396
DB 375 TTCACTTCCGCTCGGAGCAAACTTGGAAATATAA 410

RESULT 2

LOCUS BF128999 691 bp mRNA
DEFINITION 601811318F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054205 5',
mRNA sequence.
ACCESSION BF128999
VERSION BF128999.1 GI:10968039
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
JOURNAL NIH-MGC http://mgc.nci.nih.gov/
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: L1CM894 row: c column: 06
High quality sequence stop: 682.
Location/Qualifiers
1. 691
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4054205"
/lab_host="NIH_MGC_48"
/tissue="primary B-cells from tonsils (cell line)"
/note="Organ: B-cells; Vector: pOTB7; Site:1: XhoI;

FEATURES

source

Site-2: EcoRI: cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH-MGC Library."

BASE COUNT 160 a 175 c 178 g 176 t 2 others
 ORIGIN

Query Match 68.9%; Score 272.8; DB 144; Length 691;
 Best Local Similarity 80.6%; Pred. No. 2.3e-73;
 Matches 319; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

OY 1 atgattccacagccaggtcttatatgctgcgtatggtatcgtacccgtgag 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 170 ATGGTGTTCACAGACCCAGGCTTCATTCTGTTGCTCTGATCTCTGGTCCACGGG 229
 OY 61 gacattgtctgacacagctccagatccctgctgtaagttagagagagccact 120
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 230 GACATCGTATGACCCAGCTCCAGACTCCGCTGTCTCTGCGCAGAGGCGCAC 289
 OY 121 attagctgcaaatccagtgtagctgtctcaacagtagaaccgagagactactgtct 180
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 230 ATCAACTGCACTCCAGCAGAGTGTTTATATACACTCCACAAATAGAACTACTAGCT 349
 OY 181 tggtaaccagagaaccagagcgctcccttaactcgtatctactgagagcactag 240
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 350 TGTGACACAGCAAAACAGAGAGGCTCTTAAGCTGCTCATTTACTGGCANTCTACCCG 409
 OY 241 gaattcgggtccctgtagcttcagtgagtgagctcgtggagacattcactcacc 300
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 410 GAATCCGGGGTCCCTGACCGATTGAGTGCGACGCGGTCTGGAGAGATTCTACCTCACC 469.
 OY 301 atccagagctcagagcagagcagtgagctgagcttactgacagcaactatactt 360
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 470 ATCACAGAGCTTCAGAGCTGAGATGTGCGAGTTTATTTACTGTACCAATATTATAGTACT 529
 OY 361 tacacgttcgacagagagaccaaagtgagaaataaa 396
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 530 GGGACGTTGGCCAGGAGGACCAAGGTGCAATCAAA 565

RESULT 3

BG148633 300 bp mRNA EST 01-FEB-2001
 LOCUS ub5b09.v1 Soares_mouse_NMGB_bcell Mus musculus cDNA clone
 DEFINITION IMAGE:3383368 5' similar to SW:KV4C_HUMAN P06314 IG KAPPA CHAIN
 V-IV REGION B17 PRECURSOR.; mRNA sequence.

ACCESSION BG148633.1 GI:12652055
 VERSION BG148633
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 300)
 AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:1088364

FEATURES
 source
 Seq primer: -40RP from Gibco.
 Location/Qualifiers
 1..300
 /organism="Mus musculus"

/dbLxref="taxon:10090"
 /clone="IMAGE:3383368"
 /clone.lib="Soares_mouse_NMGB_bcell"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: germinal B-cell; Vector: pT73D-Pac
 (pharmacia) with a modified polylinker; Site_1: Not I;
 Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
 oligo(dT) primer [5',
 TGTACCACTGGAAGGGGAGGCGCCGCTTTTTTTTTTTTTTTTTTTTTTTT
 T 3']; double-stranded cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of the modified pT73 vector.
 Library is normalized; constructed by Bento Soares and
 M. Fatima Bonafide."

BASE COUNT 85 a 72 c 79 g 64 t
 ORIGIN

Query Match 65.3%; Score 258.6; DB 174; Length 300;
 Best Local Similarity 94.9%; Pred. No. 4.4e-69;
 Matches 278; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

OY 105 aggaagaagggccactatagctgcaaatccagtcagtgctgtcacaagtagaaccg 164
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 5 AGGAGAGAGGTCACATATGAGCTGCAAAATCCAGTCAGATCTGCTCAACAGAGACCCG 64
 OY 165 agagaactactgtgtgtaccagagaaccagagcgacctcttaactgctgacta 224
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 65 AAGAAGACTACTGCTTGTGTACACACAGAGGAGAGCTCTCTAACTGCTGATCTTA 124
 OY 225 ctggcattccactaaggaatctgggtccctgtagctgtcagtgagtgagctggagac 284
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 125 CCGGCGATTCACATAGGAGATCTGGGCTCCGATGCTTACAGAGCAGTGTGGGAC 184
 OY 285 aga-cttcaactcgcacatccagcagctgcagagcctggaagaogtggcaattactca 343
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 185 AGATTTTCACTCTCACACATGAGCTGTCAGAGCTGGAAGACCTGGCACTTTATTACTCA 244
 OY 344 cgcactctataatcttaccagcttcgacagagaggaacagtgtagaataaa 396
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 245 AGCATCTTATATCTGTATACGTTTCGAGGGGGGACCAAGCTGGAATTAATAA 297

RESULT 4

AM405821 641 bp mRNA EST 16-FEB-2000
 LOCUS UI-HF-B10-abp-b-07-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
 DEFINITION IMAGE:3057636 5', mRNA sequence.

ACCESSION AM405821
 VERSION AM405821.1 GI:6924878
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 641)
 AUTHORS NIH-MGC http://mgc.ncbi.nlm.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab
 DNA sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 www-bio.llnl.gov/bdnp/image/image.html

Seq primer: M13 Forward.

FEATURES
 source
 Location/Qualifiers
 1..641

```

/organism="Homo sapiens"
/db.xref="taxon:9606"
/clone="IMAGE:3057636"
/clone_lib="NIH_MGC_37"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab.host="DH10B (LT1)"
/notes="Vector: pT73-Pac; Site.1: NotI; Site.2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

```

```

BASE COUNT      159 a      178 c      163 g      141 t
ORIGIN
Query Match      64.6%; Score 256; DB 114; Length 641;
Best Local Similarity 81.0%; Pred. No. 3.5e-68;
Matches 311; Conservative 0; Mismatches 70; Indels 3; Gaps 1;

```

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QY 16 caggttctatatgtctgctgctataggatctgacacctgtggagacattgtgtgaca 75
    |||||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 8 CAGGCTTCATTTCTGCTGCTGCTGATCTGCTGCTACGGGACATCGATGACC 67
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 76 cagttccagattccctgctgctgaaacttagagagagggccactatgtgtcaaatcc 135
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 68 CAGTCTCCAGACTCCCTGCTGCTGCTGCGGAGAGGGCCACCATCACTGCAAGTCC 127
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 136 agtcaagactgctcaacagtagaacccagagaaactactgtgtgtacacagagaa 195
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 128 ACCGAGAGCTTTTATACAGCTCCACATPAGAACTACTACTGTTGATACAGAGAA 187
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 196 ccaggagcagctccctaactgctgactactctgggcaatcactaggaatctgggtccct 255
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 188 CAGGGGACCTCTCAAGCTGCTCATTTACTGGGCACTACCCGGCAATCCGGGGTCCCT 247
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 256 gctgcctgaatggcagtgatctggagagagattcactcaccacagcagctgcag 315
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 248 GACCGATTAGTGGACGGCGGCTGGGACAGATTTCACTCTCCATCCACACCTGACG 307
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 316 gctgaagactgtgacgttattactgacgaactccta--taactttacagcttcgga 372
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 308 GCTGAGAGATGTGGCAGATTATTTACTGTCAAGCATATTATATAGTACTCTCGAGCTTCGCG 367
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 373 caggggagccaaggtggaataaaa 396
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 368 CAGGGGACCAAGGTGGAATCAAA 391
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

RESULT 5
LOCUS AM390292 643 bp mRNA EST 04-FEB-2000

DEFINITION CM2-ST0182-221099-023-f04 ST0182 Homo sapiens cDNA, mRNA sequence.

ACCESSION AM390292

VERSION AM390292.1 GI:6894951

KEYWORDS EST

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 643)

AUTHORS HCGP <http://www.ludwig.org.br/RESTES>.

TITLE The FAPESP/LICR Human Cancer Genome Project

JOURNAL Unpublished (1999)

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
<http://www.ludwig.org.br/scripts/gethtml2.pl?rl=CM2&t2=CM2-ST0182-221099-023-f04&t3=1999-10-22&t4=1>
 Seq primer: puc 18 forward
 High quality sequence start: 7
 High quality sequence stop: 641.
 Location/Qualifiers

```

FEATURES
  source          1..643
                  /organism="Homo sapiens"
                  /db.xref="taxon:9606"
                  /clone_lib="ST0182"
                  /dev_stage="Adult"
                  /note="Organ: stomach; Vector: puc18; Site.1: SmaI;
                  Site.2: SmaI. A mini-library was made by cloning products
                  derived from ORESTES PCR (0.5. Letters Patent application
                  No. 196,716 - Ludwig Institute for Cancer Research)
                  profiles into the puc 18 vector. Reverse transcription of
                  tissue mRNA and cDNA amplification were performed under
                  low stringency conditions."
BASE COUNT      162 a      173 c      162 g      146 t
ORIGIN
Query Match      64.0%; Score 253.4; DB 114; Length 643;
Best Local Similarity 78.9%; Pred. No. 2.2e-67;
Matches 315; Conservative 0; Mismatches 81; Indels 3; Gaps 1;

```

```

QY 1 atgattcacagagccaggttcttattatgtctgtctataggtatctgtgacctgtgg 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 9 ATGCTGTGACAGACCCAGGCTCTCATTTCTGCTGCTGATCTGATCTGGTCCACGG 68
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 61 gacattgtctgacagactcctcagattccctgtcgttaagcttagagagagggcact 120
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 69 GACATCGTGTGATCCAGCTCCAGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 128
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 121 attagctgcaatccagctgacagctgctgctcaacagtagaacccagagaaactctgtgc 180
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 129 ATCACTGCAAGTCCAGCCAGAGATATTTTATACACTCCAAATATAGAACTTACTAGCT 188
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 181 tggtaacagcagaagaacagggcagcctcctaactgtgactgactcgtggcactag 240
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 189 TGGTACCAGCAGAAACAGAGACAGCTCTCAACTCTCTCTTTTACTGCGGATCTACGCG 248
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RESULT 6

LOCUS BF674779 886 bp mRNA EST 21-DEC-2000

DEFINITION 602137932F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274551 5',

ACCESSION BF674779

VERSION BF674779.1 GI:11948674

KEYWORDS EST

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 886)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)


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RESULT      8
LOCUS       BF663188
DEFINITION  60214432F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297951 5',
            mRNA sequence.
ACCESSION   BF663188
VERSION     BF663188.1
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 887)
AUTHORS     NIH-MGC http://mhc.nci.nih.gov/
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert.Strausberg@nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            CDNA Library Preparation: Ling Hong/Rubin Laboratory
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
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            High quality sequence stop: 691.
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            for average insert size 1.8kb. Library constructed by Ling
            Hong in the laboratory of Gerald M. Rubin (University of
            California, Berkeley) using ZAP-cDNA synthesis kit
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            Note: this is a NIH_MGC library."
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DEFINITION  EST363649 MAGE resequences, MAGB Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW951579
VERSION     AW951579.1
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 388)
AUTHORS     Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt
            I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.D. and
            Quackenbush, J.
TITLE       Assessment of gene expression patterns in a model of colon tumor
            metastasis using a 19,200 element cDNA microarray
JOURNAL     Unpublished (2000)
COMMENT     Contact: John Quackenbush
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 3528
            Fax: 301 838 0208
            Email: johng@tigr.org
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 VERSION AV685285.1 GI:10287148
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 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 401)
 AUTHORS Wu,T., Qian,B., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z., Zeng,L.,
 Xu,X., Li,N., Huang,Q., Kang,B., Gao,X., Xu,Z., Xiao,H.,
 Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang
 Y., Gu,Y., Chen,Z. and Han,Z.
 Homo sapiens CDNA GK-clones
 Unpublished (2000)
 TITLE Contact: Zeguang Han
 JOURNAL Chinese National Human Genome Center at Shanghai
 COMMENT 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919(ex.45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 533)
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 TITLE Contact: Simpson A.J.G.
 JOURNAL Laboratory of Cancer Genetics
 COMMENT Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LIRC Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?fl=6tz-IL5-UM0071-120.
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 Seq primer: puc 18 forward
 High quality sequence stop: 419.
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 716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
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as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGC-3'
and 3' adaptor sequence: 5'-CACGGCCATTATGGC-3'

```

Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

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OM nucleic - nucleic search, using sw model

Run on: April 29, 2001, 20:39:39 ; Search time 151.39 Seconds

(without alignments)
1527.032 Million cell updates/sec

Title: US-09-249-011-7

Perfect score: 396

Sequence: 1 atgattaccagcgccaggt.....ggaccaagtggaataaaa 396

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	396	100.0	396	21	A59695	DNA encoding light
2	360.8	91.1	396	21	A59693	Nucleotide sequence
3	340	85.9	480	10	N91663	Light chain of mon
4	332	83.8	952	16	O94036	MAB 55.1 light cha
5	301.4	76.1	439	18	T60729	CDNA encoding huma
6	301.4	76.1	439	18	T60730	CDNA encoding huma
7	298.2	75.3	399	15	O66845	Sequence encoding
8	293.6	74.1	402	18	T43415	Xenograft antibody
9	288.6	72.9	399	17	Q74067	Monoclonal antibody
10	288.6	72.9	439	18	T60734	CDNA encoding wild
11	286.8	72.4	418	17	T34152	Monoclonal antibod

12	285.4	72.1	439	18	T72268
13	285.4	72.1	460	18	T72238
14	283.2	71.5	342	20	X34465
15	279.8	70.7	1443	15	O62958
16	279	70.5	427	20	Z32779
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19	277.8	70.2	747	19	V36237
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21	275.2	69.5	660	14	O53430
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23	270.6	68.3	864	20	V72072
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25	270.6	68.3	2025	20	V72064
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32	257.4	65.0	798	14	O34842
33	255.2	64.4	423	20	X90025
34	253.6	64.0	463	21	O98443
35	250.2	63.2	407	13	O26047
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37	248.6	62.8	8068	20	Z32784
38	248.2	62.7	344	13	O30900
39	247	62.4	5703	17	T34110
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43	241.6	61.0	744	20	X77247
44	241.4	61.0	339	21	A38803
45	241.2	60.9	399	21	A28641

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	DB	ID	Description
1	A59695	396	100.0	396	21	A59695	DNA encoding light chain variable region of humanised 3S1 antibody.
2	A59695	360.8	91.1	396	21	A59693	Antibody 3D1. B7 molecule; B7: humanised immunoglobulin.
3	A59695	340	85.9	480	10	N91663	autoimmune disease; infectious disease; inflammatory disorder;
4	A59695	332	83.8	952	16	O94036	systemic lupus erythematosus; diabetes mellitus; insulin; asthma;
5	A59695	301.4	76.1	439	18	T60729	arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
6	A59695	301.4	76.1	439	18	T60730	multiple sclerosis; transplant rejection; proliferative disease;
7	A59695	298.2	75.3	399	15	O66845	leukemia; lymphoma; anemia; sickle-cell anemia; thalassemia;
8	A59695	293.6	74.1	402	18	T43415	aplastic anaemia; myeloid dysplasia syndrome; ss.
9	A59695	288.6	72.9	399	17	Q74067	Synthetic.
10	A59695	288.6	72.9	439	18	T60734	Mus sp.
11	A59695	286.8	72.4	418	17	T34152	Homo sapiens.

DNA encoding light chain variable region of humanised 3S1 antibody.

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/note= "no termination codon given"

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MO200047625-A2.

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 PF 12-FEB-1999; 99US-0249011.
 PR 24-JUN-1999; 99US-0339596.
 XX (GEMV) GENETICS INST INC.
 XX Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;
 PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;
 XX WPI; 2000-524532/47.
 DR P-PSDB; B07966.
 XX Humanized immunoglobulin having a binding specificity to B7-1 (derived
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 PT modulates immune responses and can therefore treat e.g. autoimmune
 PT diseases, infectious diseases -
 XX
 XX Example 3; Fig 2B; 162pp; English.
 XX
 CC The present sequence encodes the light chain variable region of the
 CC humanised murine antibody 3D1. The antibody has a binding specificity to
 CC B7 molecules. The antibody is used to construct humanized
 CC immunoglobulins, which comprise an antigen binding region of non-human
 CC origin and a portion of a human immunoglobulin. The humanized
 CC immunoglobulins are useful for treating autoimmune diseases, infectious
 CC diseases, inflammatory disorders, systemic lupus erythematosus, diabetes
 CC mellitus, insulinits, asthma, arthritis, inflammatory bowel disease,
 CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are
 CC also useful for treating a transplant recipient or preventing transplant
 CC rejection in a transplant recipient, and treating proliferative disease
 CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,
 CC thalassemia and aplastic anaemia), inborn errors of metabolism,
 CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
 XX
 XX Sequence 396 BP; 100 A; 96 C; 104 G; 96 T; 0 other;
 SQ

Query Match 100.0%; Score 396; DB 21; Length 396;
 Best Local Similarity 100.0%; Pred. No. 9, 8e-120;
 Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggaatcacaggccaggtctctatatactgctgctgctatggtatctggcaccctgagg 60
 |||||||
 DB 1 atgattcacaggccaggtctctatatactgctgctgctatggtatctggcaccctgagg 60
 QY 61 gaacatgctgacacagcttccagattccctggcgtgtaagcttagagagagggccact 120
 |||||||
 DB 61 gaacatgctgacacagcttccagattccctggcgtgtaagcttagagagagggccact 120
 QY 121 attagctgcaaatccagtcagatctctcaacagtagaacccgagagaactacttgct 180
 |||||||
 DB 121 attagctgcaaatccagtcagatctctcaacagtagaacccgagagaactacttgct 180
 QY 181 tgggtaccagagaagaacagggcagccctctaaactgctgtaactgtaactggaatcacc 240
 |||||||
 DB 181 tgggtaccagagaagaacagggcagccctctaaactgctgtaactgtaactggaatcacc 240
 QY 241 gaactctgggtccctgctgctcctcagtgagtgagtgatctggagacagattcactcacc 300
 |||||||
 DB 241 gaactctgggtccctgctgctcctcagtgagtgagtgatctggagacagattcactcacc 300
 QY 301 atcagcagcttgacaggttgagacgctgtattatcagcagcagcatttataatctt 360
 |||||||
 DB 301 atcagcagcttgacaggttgagacgctgtattatcagcagcagcatttataatctt 360
 QY 361 tacacgttcgacaggggagacaggttgaaataaa 396
 |||||||
 DB 361 tacacgttcgacaggggagacaggttgaaataaa 396

RESULT 2
 ID A59693 standard; DNA; 396 BP.
 XX A59693;
 AC 14-NOV-2000 (first entry)
 DT
 XX Nucleotide sequence of light chain variable region of 3S1 antibody.
 DE
 XX Antibody 3D1; B7 molecule; B7: humanised immunoglobulin;
 KW autoimmune disease; infectious disease; inflammatory disorder;
 KW systemic lupus erythematosus; diabetes mellitus; insulinits; asthma;
 KW arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
 KW multiple sclerosis; transplant rejection; proliferative disease;
 KW leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
 KW aplastic anaemia; myeloid dysplasia syndrome; ss.
 XX
 XX Mus sp.
 OS
 XX Key Location/Qualifiers
 FH 1..396
 FT CDS /*tag= a
 FT /product= "light chain variable region of 3D1 antibody"
 FT /note= "no termination codon given"
 FT sig_peptide 1..60
 FT /*tag= b
 FT mat_peptide 61..396
 FT /*tag= c
 XX
 XX WO200047625-A2.
 PN 17-AUG-2000.
 PD 09-FEB-2000; 2000MO-US03303.
 PF 12-FEB-1999; 99US-0249011.
 PR 24-JUN-1999; 99US-0339596.
 XX
 XX (GEMV) GENETICS INST INC.
 XX Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;
 PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;
 XX WPI; 2000-524532/47.
 DR P-PSDB; B07964.
 XX Humanized immunoglobulin having a binding specificity to B7-1 (derived
 PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,
 PT modulates immune responses and can therefore treat e.g. autoimmune
 PT diseases, infectious diseases -
 XX
 XX Example 1; Fig 1B; 162pp; English.
 XX
 CC The present sequence encodes the light chain variable region of the
 CC murine antibody 3D1. The antibody has a binding specificity to B7
 CC molecules. The antibody is used to construct humanized immunoglobulins,
 CC which comprise an antigen binding region of non-human origin and a
 CC portion of a human immunoglobulin. The humanized immunoglobulins are
 CC useful for treating autoimmune diseases, infectious diseases,
 CC inflammatory disorders, systemic lupus erythematosus, diabetes
 CC mellitus, insulinits, asthma, arthritis, inflammatory bowel disease,
 CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are
 CC also useful for treating a transplant recipient or preventing transplant
 CC rejection in a transplant recipient, and treating proliferative disease
 CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,
 CC thalassemia and aplastic anaemia), inborn errors of metabolism,
 CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
 XX
 XX Sequence 396 BP; 98 A; 97 C; 104 G; 97 T; 0 other;
 SQ

Query Match 91.1%; Score 360.8; DB 21; Length 396;

Best Local Similarity 94.4%; Pred. No. 3.1e-108;
Matches 374; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 atgagttacacagccaggtcttataatctgtctgtatggtatctgcaactgtgg 60
1 atgattcacagccaggtcttataatctgtctgtatggtatctgcaactgtgg 60
Db 1 atgattcacagccaggtcttataatctgtctgtatggtatctgcaactgtgg 60

QY 61 gaattgtgtacagagttctccagatccctctgctgaagcttagagagagggccact 120
61 gaattgtgtacagagttctccagatccctctgctgaagcttagagagagggccact 120
Db 61 gaattgtgtacagagttctccagatccctctgctgaagcttagagagagggccact 120

QY 121 attagctgcaaatccagctcagagctgtctcaacagtagaacccagagaaactattgtgct 180
121 attagctgcaaatccagctcagagctgtctcaacagtagaacccagagaaactattgtgct 180
Db 121 attagctgcaaatccagctcagagctgtctcaacagtagaacccagagaaactattgtgct 180

QY 181 tggtagcagagaacacagagggcagctcctaactgtctgatacttctgtggcaactagg 240
181 tggtagcagagaacacagagggcagctcctaactgtctgatacttctgtggcaactagg 240
Db 181 tggtagcagagaacacagagggcagctcctaactgtctgatacttctgtggcaactagg 240

QY 241 gaattgtgtgtccctgtatcgtctcagtgagtgatctggagagatttcaactcacc 300
241 gaattgtgtgtccctgtatcgtctcagtgagtgatctggagagatttcaactcacc 300
Db 241 gaattgtgtgtccctgtatcgtctcagtgagtgatctggagagatttcaactcacc 300

QY 301 atcagcagctctcagagctggaagacgttgcaagttacttactcagcgaacttataatctt 360
301 atcagcagctctcagagctggaagacgttgcaagttacttactcagcgaacttataatctt 360
Db 301 atcagcagctctcagagctggaagacgttgcaagttacttactcagcgaacttataatctt 360

QY 361 tacacgttcgagacagggagaccaggttggaataaa 396
361 tacacgttcgagagggagaccaggttggaataaa 396
Db 361 tacacgttcgagagggagaccaggttggaataaa 396

RESULT 3
N91663
ID N91663 standard; DNA; 480 BP.
XX
AC N91663;
XX
DT 14-MAR-1990 (first entry)
XX
DE Light chain of monoclonal antibody 6A4.
XX
KM Monoclonal antibody 6A4; light chain; Pseudomonas aeruginosa; OMP-1.
XX
FH Key Location/Qualifiers
FT CDS 37..480
FT /*tag= a
XX
PN EP338395-A.
XX
PD 25-OCT-1989.
XX
PE 12-APR-1989; 89EP-0106463.
XX
PR 19-APR-1988; 88DE-3813023.
XX
PA (BEHW) BEHRINGWERKE.
XX
PI Domdey H, Marget M, von Specht BU;
XX
DR WPI: 1989-310861/43.
DR P-PSDB; P93078.
XX
PT Monoclonal antibody to Pseudomonas aeruginosa - and DNA coding for
XX variable antibody regions.
XX
PS Claim 1; page 6; 7pp; german.
XX
CC The sequence has a variable and constant region. Monoclonal antibody 6A4
CC reacts with the OMP-1 protein of all 19 known serotypes of P.aeruginosa.
CC It is used for therapy and diagnosis of infection, and as a carrier for
CC drugs. The antibody is IgG2a subclass.

SO Sequence 480 BP; 115 A; 118 C; 135 G; 112 T; 0 other;

Query Match 85.9%; Score 340; DB 10; Length 480;
Best Local Similarity 91.2%; Pred. No. 2.1e-101;
Matches 361; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 atgattcacagccaggtcttataatctgtctgtatggtatctgcaactgtgg 60
1 atgattcacagccaggtcttataatctgtctgtatggtatctgcaactgtgg 60
Db 37 atgattcacagccaggtcttataatctgtctgtatggtatctgcaactgtgg 96

QY 61 gaattgtgtacagagttctccagatccctctgctgaagcttagagagagggccact 120
61 gaattgtgtacagagttctccagatccctctgctgaagcttagagagagggccact 120
Db 97 gaattgtgtacagagttctccagatccctctgctgaagcttagagagagggccact 156

QY 121 attagctgcaaatccagctcagagctgtctcaacagtagaacccagagaaactattgtgct 180
121 attagctgcaaatccagctcagagctgtctcaacagtagaacccagagaaactattgtgct 180
Db 157 attagctgcaaatccagctcagagctgtctcaacagtagaacccagagaaactattgtgct 216

QY 181 tggtagcagagaacacagagggcagctcctaactgtctgatacttctgtggcaactagg 240
181 tggtagcagagaacacagagggcagctcctaactgtctgatacttctgtggcaactagg 240
Db 217 tggtagcagagaacacagagggcagctcctaactgtctgatacttctgtggcaactagg 276

QY 241 gaattgtgtgtccctgtatcgtctcagtgagtgatctggagagatttcaactcacc 300
241 gaattgtgtgtccctgtatcgtctcagtgagtgatctggagagatttcaactcacc 300
Db 277 gaattgtgtgtccctgtatcgtctcagtgagtgatctggagagatttcaactcacc 336

QY 301 atcagcagctctcagagctggaagacgttgcaagttacttactcagcgaacttataatctt 360
301 atcagcagctctcagagctggaagacgttgcaagttacttactcagcgaacttataatctt 360
Db 337 atcagcagctctcagagctggaagacgttgcaagttacttactcagcgaacttataatctt 396

QY 361 tacacgttcgagacagggagaccaggttggaataaa 396
361 tacacgttcgagagggagaccaggttggaataaa 396
Db 397 cggacgttcgagtgagagaccaggttggaataaa 432

RESULT 4
O94036
ID O94036 standard; cDNA; 952 BP.
XX
AC O94036;
XX
DT 21-NOV-1995 (first entry)
XX
DE Mab 55.1 light chain cDNA.
XX
KM Antigen binding structure; complementarity determining region; CDR,
KM CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;
KM monoclonal antibody; Mab; immunotherapy; therapy; diagnosis;
KM transgenic animal; transgenic plant; antibody engineering;
KM humanized antibody; immunotoxin; ss.
XX
OS Mus sp.
XX
OS
XX
FH Key Location/Qualifiers
FT CDS 16..735
FT /*tag= a
FT sig_peptide 16..75
FT /*tag= b
FT mat_peptide 76..732
FT /*tag= c
XX
PN W09515382-A.
XX
PD 08-JUN-1995.
XX
PE 29-NOV-1994; 94MO-GB02610.
XX
PR 03-JUN-1994; 94GB-0011089.
PR 03-DEC-1993; 93GB-0024819.
XX
PA (ZENEC) ZENECAL LTD.
XX

PI Blakey DC, Boot C, Copley CG, Hall SM, Paterson DS,
 PI Rose MS, Wright AF;
 DR WPI: 1995-215262/28.
 XX P-PSDB: R76087.
 XX
 PT Antigen binding structures containing CDRs recognising the CA55.1
 PT antigen - produced by hybridomas and host cells, for use in the
 PT diagnosis and therapy of cancer
 XX
 PS Disclosure: Fig.16; 121pp; English.
 XX
 CC MAB 55.1 (BCACC 93081901) recognises the colorectal tumor-associated
 CC antigen CA55.1. CDNA's for the heavy (Q94037) and light (Q94036)
 CC chains of 55.1 were isolated, and F(ab)'₂, Fab, Fv, scFv or
 CC V-min humanized 55.1 constructs have been expressed in myeloma
 CC cells and E. coli.
 CC
 XX
 SQ Sequence 952 BP; 245 A; 268 C; 215 G; 224 T; 0 other;

Query Match 83.8%; Score 332; DB 16; Length 952;
 Best Local Similarity 89.9%; Pred. No. 1.1e-98;
 Matches 356; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 atgagttcacagccaggttcttatatgtcgtcgtcgtatggtggtacgtgtggtg 60
 DB 16 atgagttcacagccaggttcttatatgtcgtcgtcgtatggtggtacgtgtggtg 75
 QY 61 gacattgtcgtcacagcagtcctccagattccctgtgctgtatgaagtagagagagccact 120
 DB 76 gacattgtgtagtgcacagtcctccagattccctgtgctgtatgaagtagagagagc 135
 QY 121 attagctgcaaaaccagtcagagtcgtcctcaacagtagaacccagagaaactacttggt 180
 DB 136 atgagctgcaaaaccagtcagagtcgtcctcaacagtagaacccagagaaactacttggt 195
 QY 181 tggtaacagcagaagaacagggagcctcctaaactgtcatctactcgtggtacactag 240
 DB 196 tggtaacagcagaagaacagggagcctcctaaactgtcatctactcgtggtacactag 255
 QY 241 gaattcgtgggtccctcgtatcgtcagtcagtcagtcgtgagtcgtggaacattcactcc 300
 DB 256 aaattcgtgggtccctcgtatcgtcagtcagtcagtcgtgagtcgtggaacattcactcc 315
 QY 301 atcagcagctcgtcagagctgaagacgtgagcagttattactcagcgaacttatactt 360
 DB 316 atcagcagctcgtcagagctgaagacgtgagcagttattactcagcgaacttatactt 375
 QY 361 tacacgttcggaacagggagccaaagtggaataaaa 396
 DB 376 cggagctcgtgtgagagcaccacagctggaataaaa 411

RESULT 5
 T60729
 ID T60729 standard; CDNA: 439 BP.
 XX
 AC T60729;
 XX
 DT 25-SEP-1997 (first entry)
 DE
 XX CDNA encoding humanised murine anti-E-selectin antibody CY1788V(LA).
 XX
 KM Humanised; murine; mouse; E-selectin; antibody; light chain;
 KM variable region; detection; inhibition; mediation; cell adhesion;
 KM diagnosis; reduction; inflammation; septic shock; ARDS; sepsis;
 KM acute respiratory distress syndrome; gross cystic breast disease;
 KM cancer; treatment; splanchmic occlusion shock; psoriasis;
 KM complement; chimeric; ds.
 XX
 OS Chimeric - Mus spp.
 OS Chimeric - Homo sapiens.

OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 16..426
 FT /tag= a
 FT /note= "no stop codon given"

XX W09640942-A1.
 XX 19-DEC-1996.
 XX
 XX 06-JUN-1996; 96WO-US09204.
 XX
 XX 07-JUN-1995; 95US-0482112.
 XX
 XX (CYTE-) CYTEL CORP.
 XX
 PI Bendig MM, Jones ST, Perez C, Saldanha JW, Williams MA;
 PI Jones S;
 DR WPI: 1997-077272/07.
 XX P-PSDB: W10544.
 XX
 PT Humanised anti-E-selectin antibody - useful for diagnosis and
 PT treatment of, e.g. inflammatory responses, septic shock, acute
 PT respiratory distress syndrome or cancer
 XX
 PS Claim 29; Page 69; 89pp; English.

XX The present sequence encodes the humanised murine anti-E-selectin
 CC antibody (Ab) light chain variable region, CY1788V(LA). The Ab can
 CC be used to detect E-selectin, or inhibit E-selectin mediated cell
 CC adhesion. It can also be used to diagnose, reduce or inhibit an
 CC inflammatory response, or the severity of pathologies, e.g. septic
 CC shock, acute respiratory distress syndrome, wound associated
 CC sepsis, gross cystic breast disease or cancer, or treat, e.g.
 CC splanchic occlusion shock, or psoriasis. It can be administered to
 CC a human without inducing an immune response. In addition, the
 CC effector portion of the Ab can interact with various components of
 CC the human immune system, including complement.

SQ Sequence 439 BP; 106 A; 110 C; 117 G; 106 T; 0 other;

Query Match 76.1%; Score 301.4; DB 18; Length 439;
 Best Local Similarity 86.5%; Pred. No. 8.1e-89;
 Matches 345; Conservative 0; Mismatches 51; Indels 3; Gaps 1;

QY 1 atgattcacagccaggttcttatatgtcgtcgtcgtatggtggtacgtgacactgtgg 60
 DB 28 atgagtcgaagtcctcagtcagtcctcagtcgtcgtcgttctgtggtatcgtgacactgtgg 87
 QY 61 gaattcgtgtgacacagtcctcagtcgtcgtcgtcgttctgtggtatcgtgacactgtgg 120
 DB 88 gaattcgtgtgacacagtcctcagtcgtcgtcgtcgttctgtggtatcgtgacactgtgg 147
 QY 121 attagctgcaaaaccagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 180
 DB 148 atcaactgcaagtcctcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 207
 QY 181 tggtaacagcagaagaacagggagcctcctaaactgtgatactcgtggtacactag 240
 DB 208 tggtaacagcagaagaacagggagcctcctaaactgtgatactcgtggtacactag 267
 QY 241 gaattcgtgggtccctcgtatcgtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 300
 DB 268 gaattcgtgggtccctcgtatcgtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 327
 QY 301 atcagcagctcgtcagagctgaagacgtgagcagttattactcagcagcaatctata--at 357
 DB 328 atcagcagctcgtcagagctgaagacgtgagcagttattactcagcagcaatctataatagttat 387
 QY 358 cttaacagcttcggaacagggagccaaagtggaataaaa 396

XX XX cDNA encoding wild type murine anti-E-selectin antibody CY1787V(L).
DE Humanised; murine; mouse; E-selectin; antibody; light chain;
XX variable region; detection; inhibition; mediation; cell adhesion;
KW diagnosis; reduction; inflammation; septic shock; ARDS; sepsis;
KW acute respiratory distress syndrome; gross cystic breast disease;
KW cancer; treatment; splanchic occlusion shock; psoriasis;
KW complement; ds.
XX
XX Mus spp.
OS
FH Key Location/Qualifiers
FT CDS 16..426
FT /*tag= a
FT /note= "no stop codon given"
XX
XX MO9640942-A1.
XX
XX 19-DEC-1996.
XX
XX 06-JUN-1996; 96WO-US09204.
XX
XX 07-JUN-1995; 95US-0482112.
XX
XX (CYTE-) CYTEL CORP.
XX
XX Bendig MM, Jones ST, Perez C, Saldanha JW, Williams MA;
PI Jones S;
XX
XX WPI: 1997-077272/07;
DR P-PSDB; WI0547.
XX
XX Humanised anti-E-selectin antibody - useful for diagnosis and
PT treatment of, e.g. inflammatory responses, septic shock, acute
PT respiratory distress syndrome or cancer
XX
XX Example II; Page 55; 89pp; English.
XX
XX The present sequence encodes the wild type murine anti-E-selectin
CC antibody (Ab) light chain variable region, CY1787V(L), which was
CC used in the preparation of the humanised anti-E-selectin Ab light
CC chain variable regions, CY1788V(LA-B). The humanised Ab can
CC be used to detect E-selectin, or inhibit E-selectin mediated cell
CC adhesion. They can also be used to diagnose, reduce or inhibit an
CC inflammatory response, or the severity of pathologies, e.g. septic
CC shock, acute respiratory distress syndrome, wound associated
CC sepsis, gross cystic breast disease or cancer, or treat, e.g.
CC splanchic occlusion shock, or psoriasis. They can be administered
CC to a human without inducing an immune response, in addition, the
CC effector portion of the Ab can interact with various components of
CC the human immune system, including complement.
XX
XX Sequence 439 BP; 108 A; 110 C; 116 G; 105 T; 0 other;

Query Match 72.9%; Score 288.6; DB 18; Length 439;
Best Local Similarity 84.5%; Pred. No. 1.2e-84;
Matches 337; Conservative 0; Mismatches 59; Indels 3; Gaps 1;
OY 1 atgagttcacagccaggtcttatatgtctgtcgtataggtatctggcacctgtgg 60
DB 28 atgagttcacagccaggtcttatatgtctgtcgtataggtatctggcacctgtgg 87
OY 61 gacattgtgtcgtacacagcttccagatccctgctgttaagcttggagagagccact 120
DB 88 gacattgtgtcgtacacagcttccagatccctgctgttaagcttggagagagccact 147
OY 121 attactgcaaatccagtcagagctgtctcacaacagtagaaccggagagaacttggct 180
DB 148 atgagctcgaagtcacagtcagagctgtctcacaacagtagaaccggagagaacttggct 207
OY 161 tggtagcagcagaacccagcgagcctcctaactgctgaltactgtgcatccactag 240

DB 208 tggtagcagcagaacccagcgagcctcctaactgctgaltactgtgcatccactag 267
OY 241 gaatctggggtccctgatgcgttcagtgcaatgcgtggacagatctcactcacc 300
DB 268 gaatctggggtccctgatgcgttcagtgcaatgcgtggacagatctcactcacc 327
OY 301 atcagcagctcgcagcgtgaagacgttgcagatttactgcacgcaatctata--at 357
DB 328 atcagcagctcgcagcgtgaagacgttgcagatttactgcagaaatgattatag 387
OY 358 ctctacagcttcggacaggggaccaaagttggaataaaa 396
DB 388 ccgctcagctcgtgctgtggaccaaagttggaataaaa 426
RESULT 11
T34152
ID T34152 standard; DNA; 418 BP.
XX
XX T34152;
AC
XX
XX 14-FEB-1997 (first entry)
XX
XX Monoclonal antibody PA1-3F10 variable light chain-encoding DNA.
DE
XX PA1-3F10; antibody; hybridoma; LMBP1322CB; cancer; target; epitope;
KW killing; colorectal; lung; ovary; cytotoxin; neoplasia; ss.
XX
XX Mus musculus.
OS
XX
XX Key Location/Qualifiers
FH Key 2..418
FT CDS /*tag= a
FT /note= "no start or stop codon"
XX
XX W09622310-A1.
XX
XX 25-JUL-1996.
PD
XX
XX 15-JAN-1996; 96WO-SE00029.
PF
XX
XX 18-JAN-1995; 95SE-0000148.]
XX
XX (BIOI-) BIOINVENT INT AB.
XX
XX Carlsson R, Jansson B;
PI
XX
XX WPI: 1996-354478/35.
DR
XX
XX P-PSDB; R99469.
DR
XX
XX Monoclonal antibody PA1-3F10 produced by hybridoma BCM LMBP1322CB -
PT useful to target cancer cells for killing or detection
XX
XX Claim 10; Fig 10; 62pp; English.
XX
XX T34152 encodes the variable light (VL) chain of monoclonal antibody
CC PA1-3F10 produced by hybridoma BCM LMBP1322CB. The antibody is
CC directed against an epitope present on cancer cells, in particular
CC breast, ovary, lung and colorectal cancer cells. The antibody is
CC useful for detecting cancer cell epitopes and hence in the diagnosis
CC of cancer. The antibody can be conjugated to a cytotoxic compound and
CC targeted to cancer cells to kill them.
XX
XX Sequence 418 BP; 102 A; 100 C; 107 G; 109 T; 0 other;

Query Match 72.4%; Score 286.8; DB 17; Length 418;
Best Local Similarity 84.8%; Pred. No. 4.7e-84;
Matches 334; Conservative 0; Mismatches 57; Indels 3; Gaps 1;
OY 6 ttcaagggccaggtcttatatgtctgtcgtataggtatctggcacctgtgggaat 65

PF 25-OCT-1996: 96EP-0117154.
 XX
 PR 06-NOV-1995: 95EP-0117407.
 XX
 PA (MERCK) MERCK PATENT GMBH.
 XX
 PI Bendig M, Jones T, Saldana J;
 XX WPI: 1997-334904/31.
 DR P-PSDB: W21653.
 XX
 PT Humanised form of murine monoclonal antibody Mab 15 - useful for
 XX treating lung cancer
 PS
 Claim 14: Fig 1: 71pp: English.
 CC This cDNA sequence encodes the light chain variable region VL
 CC (W21653) of murine monoclonal antibody (Mab) 15 (DSM ACC2117),
 CC a Mab that shows a therapeutic effect on human tumour cells,
 CC especially human lung cancer. The clone was isolated from
 CC hybridoma cDNA using a degenerate leader sequence primer (T72239)
 CC and a kappa constant region reverse primer (T72240). The VH region
 CC (see T72267) was also amplified. The VL and VH sequences were
 CC used in a claimed process for the production of novel humanised,
 CC reshaped Mab 15 having humanised, reshaped VL and VH sequences
 CC (see W21651 and W21652), which can be used for treating tumours,
 CC especially lung cancer, and for the manufacture of a drug related
 CC to tumours, especially lung cancer.
 XX
 SQ Sequence 460 BP; 112 A; 118 C; 113 G; 117 T; 0 other;

Query Match 72.1%; Score 285.4; DB 18; Length 460;
 Best Local Similarity 84.0%; Pred. No. 1.4e-83;
 Matches 335; Conservative 0; Mismatches 61; Indels 3; Gaps 1;
 QY 1 atgagatcacagagccaggtcttataatgctgctgctatggtatgctgacctgtggg 60
 DB 13 atgagatcacatccctggtcttataatgctgctgctatggtatgctgacctgtggg 72
 QY 61 gacatgctgctgacagctccagatctccctgctgctgctgctgctgctgctgctgctgct 120
 DB 73 gacatgctgctgacagctccagatctccctgctgctgctgctgctgctgctgctgctgct 132
 QY 121 atgagctgaatcagctcagctcagctcagctcagctcagctcagctcagctcagctcagct 180
 DB 133 atgagctgcaagctcagctcagctcagctcagctcagctcagctcagctcagctcagctcagct 192
 QY 181 tggctacagcagaacacagcagctcctctaaactgctgctgctgctgctgctgctgctgctgct 240
 DB 193 tggctacagcagaacacagcagctcctctaaactgctgctgctgctgctgctgctgctgctgct 252
 QY 241 gaatctggggtccctgctcagctcagctgctgctgctgctgctgctgctgctgctgctgctgct 300
 DB 253 gaatctggggtccctgctcagctcagctcagctcagctcagctcagctcagctcagctcagctcagct 312
 QY 301 atcagcagctcagcagctcagcagctcagcagctcagcagctcagcagctcagcagctcagcagct 357
 DB 313 atcagcagctcagcagctcagcagctcagcagctcagcagctcagcagctcagcagctcagcagct 372
 QY 358 ccttaccagctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 396
 DB 373 ccttaccagctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 411

RESULT 14
 X34465
 ID X34465 standard; cDNA: 342 BP.
 XX
 AC X34465;
 XX
 DT 25-JUN-1999 (first entry)
 XX

DE Mouse Mab 6A4 light chain variable region encoding DNA.
 XX
 XX Rolling template; nucleic acid synthesis; polynucleotide polymerase;
 KW gene production; primer; monoclonal antibody; 6A4; ss.
 XX
 XX Mus sp.
 OS
 PN WO9914370-A1.
 XX
 PD 25-MAR-1999.
 XX
 PF 15-SEP-1998: 98WO-US19157.
 XX
 PR 15-SEP-1997: 97US-0929856.
 XX
 PA (HIAT/) HIAT A C.
 PA (ROSE/) ROSE F D.
 XX
 PI Hiatt AC, Rose FD;
 XX
 DR WPI: 1999-244045/20.
 DR P-PSDB: Y06830.
 XX
 PT Producing specific polynucleotides using rolling templates
 XX
 Example 6: Page 40: 109pp: English.

The invention relates to a method for producing polynucleotides having a defined sequence using rolling templates that successively add nucleotides (nts) to a longer primer strand. The method comprises: (i) incubating, under annealing conditions, a primer and a template that has a 5'-region not complementary to the primer, a 3'-region complementary to the 3'-end of primer and a non-reactive 3'-terminus, with the template being shorter than the primer; (ii) reacting the primer with at least one nt in presence of a template-dependent polynucleotide polymerase to extend it by at least one nt (complementary to the 5'-region of template) at its 3'-end; (iii) separating the template and the extended primer; and (iv) repeating the cycle of (i)-(iii) as often as needed to synthesize the desired polynucleotide. The method is especially used to produce genes or their segments. The method provides fast, accurate, inexpensive synthesis of RNA or DNA and is more efficient than chemical coupling processes. It has higher specificity and eliminates the need for deprotection. The products can be cloned directly. The method avoids problems of waste disposal and includes an inherent editing effect (failure sequences will not be extended further in subsequent rounds) so that purification of the end product is facilitated. Synthesis may take place on a vector, simplifying cloning and sequences with codon usage optimized for a particular host can be prepared. This represents the nucleotide sequence of the light chain variable region of the mouse monoclonal antibody (Mab) 6A4, synthesised by the method of the invention.

Query Match 71.5%; Score 283.2; DB 20; Length 342;
 Best Local Similarity 90.2%; Pred. No. 6.4e-83;
 Matches 303; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
 QY 61 gacatgctgctgacacagctccagatctccctgctgctgctgctgctgctgctgctgctgct 120
 DB 1 gacatgctgctgacacagctccagatctccctgctgctgctgctgctgctgctgctgctgct 60
 QY 121 atgagctgaatcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctcagct 180
 DB 61 atgagctgaatcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctcagct 120
 QY 181 tggctacagcagaacacagcagctcctctaaactgctgctgctgctgctgctgctgctgctgct 240
 DB 121 tggctacagcagaacacagcagctcctctaaactgctgctgctgctgctgctgctgctgctgct 180
 QY 241 gaatctggggtccctgctcagctcagctgctgctgctgctgctgctgctgctgctgctgctgct 300

Db, 181 gaatctggtggtccctgacgtcctcacagcagtgatctggtgacagattcactcacc 240
QY 301 atcagcagctcgtcagcgtcgaagacggtgagttattacgcgcgaatttatactt 360
Db 241 atcagcagctcgtcagcgtcgaagacggtgagttattacgcgcgaatttatactt 300
QY 361 tacacgttcgacaggggacccaaggtcggaataaa 396
Db 301 cggacgtctcggtgagcaccacagctggaatacaa 336
RESULT 15
Q62958
ID Q62958 standard; DNA; 1443 BP.
XX
AC Q62958;
XX
DT 09-SEP-1994 (first entry)
XX
DE Glycophorin antibody IC3 Fab coding region.
XX
KM Glycophorin; antibody IC3; target binding polypeptide; PCR;
KW polymerase chain reaction; primer; antibody engineering;
XX humanized antibody; phagemid pHFA; plasmid p569;ss.
OS Synthetic.
XX
PN WO9407921-A.
XX
PD 14-APR-1994.
XX
PF 24-SEP-1993; 93WO-AU00491.
XX
PR 25-SEP-1992; 92AU-0004973.
XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
PI Atwell JL, Colman PM, Hudson PJ, Irving RA, Kortt A;
PI Lah M, Malbyrl, Power BE;
XX
DR WPI; 1994-135515/16.
XX
PR New target-binding polypeptide(s) used for diagnosis, etc. -
PR having a stable core polypeptide region with at least one
PR target-binding region covalently attached, opt. mutated to alter
PR specificity, etc.
XX
PS Disclosure; Page 42; 67pp; English.
XX
CC PCR primers given in 062951-52 were used to clone anti-glycophorin
CC antibody IC3 Fab coding region. The DNA sequence of the first 1443
CC bases of the Fab fragment in pHFA, ready for ligation post PCR
CC amplification for ligation into p569, is given in 062958.
XX
SQ Sequence 1443 BP: 391 A; 388 C; 351 G; 313 T; 0 other;
Query Match 70.7%; Score 279.8; DB 15; Length 1443;
Best Local Similarity 84.6%; Pred. No. 1.5e-81;
Matches 314; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 206 ctctaaactgctgacttacttgggcatccactaggggaatctgggtccctgacgttca 265
Db 914 ctctaaaccgctgacttacttgggcatccactaggggaatctgggtccctgacgttca 973
QY 266 gttgcagttgatacttgagacagatttcactctcaccatcagcagctcgaagacg 325
Db 974 cagcagtgatctgagacagatttcactctcaccatcagcagctcgaagacg 1033
QY 326 tggcagtttacttgcagcgaatctataatcttcaacgttcgagacagggacgaag 385
Db 1034 tggcagtttacttgcagcgaatctataatcttgcagcgttcggtgagacgaagc 1093
QY 386 tgggaataaaa 396
Db 1094 tgggaatlaaa 1104

Search completed: April 29, 2001, 20:39:41
Job time: 3488 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2001, 09:39:40 ; Search time 24.35 Seconds
(without alignments)
372.543 Million cell updates/sec

Title: US-09-249-011-8

Perfect score: 681

Sequence: 1 MDSQAQVLLILLWVSGTGC.....YCTOSYNLYTFEGGKVEIK 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR_67:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	596	87.5	133	2 PS0023	Ig kappa chain pre
2	558.5	82.0	134	1 K4HUI7	Ig kappa chain pre
3	558	81.9	120	2 G33932	Ig kappa chain pre
4	553.5	81.3	134	2 S49531	anti-Sm antibody V
5	552	81.1	133	1 K4HUI7	Ig kappa chain pre
6	542.5	79.7	138	2 S26040	Ig kappa chain pre
7	541.5	79.5	145	2 PL0014	Ig kappa chain pre
8	539.5	79.2	134	2 PC1214	Ig kappa chain pre
9	536.5	78.8	135	2 S38807	Ig kappa chain pre
10	536	78.7	138	2 A53261	Ig kappa chain pre
11	535.5	78.6	129	2 S40347	Ig kappa chain - h
12	532.5	78.2	240	2 S06084	Ig kappa chain pre
13	528.5	77.6	132	2 S46373	Ig kappa chain pre
14	515.5	75.7	134	2 S21917	Ig kappa chain V-J
15	515	75.6	121	1 K4HU	Ig kappa chain V r
16	510	74.9	113	2 PT0407	Ig kappa chain pre
17	506.5	74.4	120	2 S51147	Ig light chain V r
18	506.5	74.4	124	2 S40364	antibody light cha
19	506	74.3	112	2 S43103	Ig kappa chain - h
20	502.5	73.8	113	2 S34002	Ig kappa chain V-J
21	500.5	73.5	136	2 A49137	Ig kappa chain V r
22	497.5	73.1	114	1 K4HUI7	Ig kappa chain pre
23	494	72.5	112	2 PL0265	Ig kappa chain V-I
24	493.5	72.5	129	2 S40329	Ig kappa chain V-J
25	492	72.2	113	2 PT0408	Ig kappa chain V r
26	490.5	72.0	113	2 S30520	Ig light chain V r
27	482	70.8	112	2 S41393	Ig kappa chain V r
28	480	70.5	103	2 PH1047	Ig kappa chain V r
29	476.5	70.0	113	2 S34003	Ig kappa chain V r

30	475	69.8	103	2 PH1052	Ig light chain V r
31	473.5	69.5	111	2 S03304	Ig kappa chain V r
32	473.5	69.5	114	2 S44116	Ig kappa chain V-J
33	473.5	69.5	114	2 S44119	Ig kappa chain V-J
34	471	69.2	104	2 PH1101	Ig light chain V r
35	470.5	69.1	113	2 S30523	Ig kappa chain V r
36	470	69.0	104	2 PH1102	Ig light chain V r
37	467	68.6	103	2 PH1051	Ig light chain V r
38	466	68.4	104	2 PH1104	Ig light chain V r
39	464	68.1	103	2 PH1050	Ig light chain V r
40	462.5	67.9	113	2 PL0263	Ig kappa chain V r
41	460	67.5	101	2 PH1046	Ig light chain V r
42	457	67.1	104	2 PH1103	Ig light chain V r
43	452.5	66.4	113	2 PL0264	Ig kappa chain V r
44	452.5	66.4	214	2 S68212	Ig kappa chain V r
45	452	66.4	106	2 A49138	Ig kappa chain V r

ALIGNMENTS

RESULT 1
PS0023
Ig kappa chain precursor V region (6A4) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jun-1990 #sequence_rev150 07-Jun-1990 #text_change 21-Jan-2000
C:Accession: PS0023
R:Margel, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Domkey, H.
Gene 74, 335-345, 1988
A:Title: Cloning and characterization of cDNAs coding for the heavy and light chains
A:Reference number: PS0023; M01D:89232725
A:Accession: PS0023
A:Molecule type: mRNA
A:Residues: 1-133 <MAR>
A:Experimental source: strain BALB/c
A:Note: the amino-terminal four residues of the mature protein were directly sequence
C:Comment: This chain was obtained from a monoclonal antibody against Pseudomonas aer
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-133/Product: Ig kappa chain V region 6A4 #status experimental <IGV>
F:36-116/Domain: immunoglobulin homology <IMV>

Query Match 87.5%; Score 596; DB 2; Length 133;
Best Local Similarity 86.4%; Pred. No. 8.6e-44;
Matches 114; Conservative 10; Mismatches 8; Indels 0; Gaps 0;
QY 1 MDSQAQVLLILLWVSGTGDIVLTOSPDLSVLSGERATISCKSSQSLNSRTRENYLA 60
|||||
Db 1 MDSQAQVLLILLWVSGTGDIVWSQSPSLAVSAGKVTWCKSSQSLNSITRKFLLA 60
QY 61 WYQKPGQPKLLIYMASTRSGVDFRSGSGSTDFLTITSSLAQADVAVYCTOSYNL 120
|||||
Db 61 WYQKPGQPKLLIYMASTRSGVDFRFTGSGSTDFLTITSSVQADLAIVYCKQSYNL 120
QY 121 YTFEGGKVEIK 132
|||
Db 121 RTFEGGKVEIK 132
RESULT 2
K4HUI7
Ig kappa chain precursor V-IV region (B17) - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_rev150 30-Jun-1987 #text_change 21-Jan-2000
C:Accession: A01905
R:Marsh, P.; Mills, F.; Gould, H.
Nucleic Acids Res. 13, 6531-6544, 1985
A:Title: Detection of a unique human V kappa germline gene by a cloned cDNA probe.
A:Reference number: A01905; M01D:86041854
A:Accession: A01905
A:Molecule type: mRNA

A:Residues: 1-134 <MAR>
A:Note: the sequence was determined from the differentiated gene
A:Note: the authors translated the codon TGC for residue 76 as Trp
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into tetramers.
C:Superfamily: immunoglobulin v region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
E:1-20/Domain: signal sequence #status predicted <SIG>
E:21-134/Product: Ig kappa chain v-IV region (B17) #status predicted <MAT>
F:21-43/Region: framework 1
F:36-116/Domain: immunoglobulin homology <IMW>
F:44-60/Region: complementarity-determining 1
F:61-75/Region: framework 2
F:76-82/Region: complementarity-determining 2
F:83-114/Region: framework 3
F:115-121/Region: complementarity-determining 3
F:122-134/Region: framework 4
F:43-114/Disulfide bonds: #status predicted

Query Match	82.0%;	Score 558.5;	DB 1;	Length 134;
Best Local Similarity	85.4%;	Pred. NO. 1.3e-40;		
Matches 11;	Conservative 6;	Mismatches 12;	Indels 1;	Gaps 1

QY 4 QAQVILLLLLWVGTCGDIVLTQSPDSLAVSLGERATISCSQSQSLNSTRREYLAHQ 63
| | | | | : | | | | | : | | | | | : | | | | |
DB 4 QTQVFISLLMISGAVDIVMTQSPDSLAVSLGERATINCKSSQSLYSSDNKNYLAHQ 63

```
Qy      64 QKPGQPCKLLIYMASTRSGVPDRFSSGSGTFTLTISLQAEDVAVYYCTOSYN-YT 122
        ||||| | | | | | | | | | | | | | | | | | | | | | : |
Db      64 QKPGQPCKLLIYCASTRSGVPDRFSSGSGTFTLTISLQAEDVAVYYCQYINLPWT 123
```

QY	123	EGQGTKEIK	132
Db	124	EGQGTKEIK	133

RESULT 3
G33932
The blood serum of series (D33) - mouse

C/Species: Mus musculus (house mouse)
C/Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C/Accession: G33932
R/Bacala, R.; Yo Quang, T.; Gilbert, M.; Terrynek, T.; Avrameas, S.
Read Set in e 7 of 4574/4580 1000

A:Title: Two murine natural polyelectrolyte antibodies are encoded by nonmutated germ-line genes
A:Reference number: A33932, PMID:89282823

A:Status: preliminary; not compared with conceptual translation
A:molecule type: mRNA

A;Residues: 1-120 <BAC>

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-116/Domain: immunoglobulin homology <Imm>

Query Match	81.9%	Score 558	DB 2	length 120
Best Local Similarity	88.3%	Pred. No. 1.3e+40		
Matches 106	Conservative	8	Mismatches 6	Indels 0
				Gaps 0

QY	1	MDSPAQVILLILLLLWVSGTCGDIVLTQSPDPSILAVSLGERATITSCCKSSQSLNLSRTRENYLA	60
QY	1	MDSPAQVILLILLLLWVSGTCGDIVLTQSPDPSILAVSLGERATITSCCKSSQSLNLSRTRENYLA	60
Db	1	MDSPAQVILLILLLLWVSGTCGDIVLTQSPDPSILAVSLGERATITSCCKSSQSLNLSRTRENYLA	60
QY	61	WYQKPCGPKLLIYMASTRESGVPDRFSGSGCTDITLTITSSIAQDAVAVVYCTQSYNL	120
QY	61	WYQKPCGPKLLIYMASTRESGVPDRFSGSGCTDITLTITSSIAQDAVAVVYCTQSYNL	120
Db	61	WYQKPCGPKLLIYMASTRESGVPDRFSGSGCTDITLTITSSIAQDAVAVVYCTQSYNL	120

RESULT : 4
S49531
anti- κ m antibody VL chain (V kappa 4/J kappa 3) - human
C:Species: Homo sapiens (man)

```

C:Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Jan-2000
C:Accession: S49531
R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
  submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-5m autoantib
A:Reference number: S48797
A:Accession: S49531
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-134 <MAH>
A:Cross-references: EMBL:Z46347; NID:G560841; PIDN:CAA86466.1; PID:G560842
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
F:36-116/Domain: immunoglobulin homology <IMH>

```

Query Match	81.3%	Score 553.5;	DB 2;	Length 134;
Best Local Similarity	83.1%;	Pred. No. 3.4e-40;		
Matches 108; Conservative	8;	Mismatches 13;	Indels 1;	Gaps 1;

4 QTOVFISLLWISGAGDIWMQSPDSLAVSLGERATINCCKSSQSVLYSSNNKNYLAWYQ 63

```

64 QKPGCPKLLIYMASTRSGVPDRFSGSSGTDTLTLTSSLAQEDVAVYYCCOQYSTAFT 122

```

Db	124	EGPGTKVDIK	133
----	-----	------------	-----

RESULT 5 —
KAKUJI —
Ig kappa chain precursor, V-IV region (J1) - human

C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 21-Jan-2000
C/Accession: A01904
R/Klloeck, H.G.; Bornkamm, G.W.; Combrinato, G.; Mockkat, R.; Pohlentz, H.D.;

A:Title: Subgroup IV of human immunoglobulin K light chains is encoded by a single gene
A:Reference number: A93589; MUID:86041853
A:Accession: A01904
A:Molecule type: DNA

A:Note: the sequence was determined from the differentiated gene

C;Genetics:
A;Gene: GDB:IGKV
A;Cross-references: GDB:119341; OMIM:146980

A;Map position: 2p12-2p1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (A) and two identical heavy (B) polypeptide chains. The chains are held together by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into a higher order structure.

F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-133/Product: Ig kappa chain V-IV region (JI) #status predicted <MAT>
F:21-43/Region: framework 1

F 36-116/Domain: immunoglobulin homology <IMH>
F 44-60/Region: complementarity-determining 1
F 61-75/Region: framework 2
F 76-82/Region: complementarity-determining 2
F 83-114/Region: framework 3
F 115-122/Region: complementarity-determining 3
F 123-133/Region: framework 4
F 43-114/Disulfide bonds: #status predicted

Query Match	81.1%;	Score 552;	DB 1;	length 133;
Best Local Similarity	83.7%;	Pred. No. 4.5e-40;		
Matches 108;	Conservative 6;	Mismatches 15;	Indels 0;	Gaps 0;

QY 0A0VLLILLMWSGTCGDIYLTQSPDSLAVSLGERATISCKSSQSLNSRTRENTLAWQ 63
 DB 4 QTVGVLSLLMISGAYGDIYMTQSPDSLAVSLGERATINCKSSQSLNSRTRENTLAWQ 63
 QY 64 QKRGQPKLLIYASTRESGVPPDRFSGSGGTDTFTLTISLQAEVAVVYCTQSYNLVYF 133
 DB 64 QKRGQPKLLIYASTRESGVPPDRFSGSGGTDTFTLTISLQAEVAVVYCTQSYNLVYF 123
 QY 124 GGGTKEIK 132
 DB 124 GGGTKEIK 132

RESULT 6

S26040
 Ig kappa chain precursor - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 21-Jan-2000
 C:Accession: S26040; S78098
 R:Okamoto, M.; Honjo, T.
 Nucleic Acids Res. 18, 1895, 1990
 A:Title: Nucleotide sequences of the gene/cDNA coding for anti-murine erythrocyte autocal
 A:Reference number: S09216; M0ID:90245389
 A:Accession: S26040
 A:Molecule type: DNA
 A:Residues: 1-138 <OK>
 A:Cross-References: EMBL:X51742
 A:Note: the authors translated the codon ACC for residue 107 as Thr and AGT for residue
 R:Okamoto, M.
 submitted to the EMBL Data Library, February 1990
 A:Reference number: S78098
 A:Accession: S78098
 A:Molecule type: DNA
 A:Residues: 1-87, 'W', 89-138 <OK>
 A:Cross-References: EMBL:X51742; NID:952697; PIDN:CAA36032.1; PID:952698
 C:Genetics: 22/1
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-138/Product: Ig kappa chain (fragment) #status predicted <MAT>
 F:41-121/Domain: immunoglobulin homology <IM>

Query Match 79.7%; Score 542.5; DB 2; Length 138;
 Best Local Similarity 75.2%; Pred. No. 3e-39;
 Matches 103; Conservative 17; Mismatches 12; Indels 5; Gaps 1;
 QY 1 MDSQAQVLLILLMWSG----TCGDIYLTQSPDSLAVSLGERATISCKSSQSLNSRTR 55
 DB 1 MDSQAQVLLILLMWSGEKFSTCGDIYMSQSSSLTVSGEYVTKMCKSSQSLNSNMQ 60
 QY 56 ENYLAHYQKPGQPKLLIYASTRESGVPPDRFSGSGGTDTFTLTISLQAEVAVVYCT 115
 DB 61 KNYLAHYQKPGQPKLLIYASTRESGVPPDRFSGSGGTDTFTLTISVVAEDLAVVFCQ 120
 QY 116 QSYNLYTFGGTKEIK 132
 DB 121 QYSYNLYTFGGTKEIK 132

RESULT 7

PL0014
 Ig kappa chain precursor V region (F6-3) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
 C:Accession: PL0014
 R:Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieffer-Emmons, T.; Kohler, H.
 Mol. Immunol. 25, 33-40, 1988
 A:Title: Structural basis of stimulatory anti-idiotypic antibodies.
 A:Reference number: PL0011; M0ID:88142863
 A:Accession: PL0014
 A:Molecule type: mRNA

A:Residues: 1-145 <CHE>
 A:Experimental source: cell line F6-3
 C:Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphoryl
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-134/Product: Ig heavy chain V region (4C11) #status predicted <MAT>
 F:36-116/Domain: immunoglobulin homology <IM>
 F:44-60/Region: complementarity-determining 1
 F:76-82/Region: complementarity-determining 2
 F:115-123/Region: complementarity-determining 3
 F:135-145/Domain: constant region (fragment) #status predicted <COR>

Query Match 79.5%; Score 541.5; DB 2; Length 145;
 Best Local Similarity 77.6%; Pred. No. 3.8e-39;
 Matches 104; Conservative 18; Mismatches 9; Indels 3; Gaps 2;
 QY 1 MDSQAQVLLILLMWSGTCGDIYLTQSPDSLAVSLGERATISCKSSQSLNSRTRENTLAWQ 60
 DB 1 MDSQAQVLLILLMWSGTCGDIYMSQSSSLTVSGEYVTKMCKSSQSLNSNMQNFIA 60
 QY 61 WYQKPGQPKLLIYASTRESGVPPDRFSGSGGTDTFTLTISLQAEVAVVYCTQSYNL 120
 DB 61 WYQKPGQPKLLIYASTRESGVPPDRFSGSGGTDTFTLTISVVAEDLAVVYCTQSYNL 119
 QY 121 Y--TFGGTKEIK 132
 DB 120 YPLTFGGTKEIK 132

RESULT 8

PC1214
 Ig kappa chain precursor V region (mAb H8) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
 C:Accession: PC1214
 R:Hong, H.J.; Kim, A.K.; Ryu, C.J.; Park, S.S.; Chung, H.K.; Kwon, K.S.; Kim, K.L.; K
 Gene 121, 331-335, 1992
 A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a
 A:Reference number: PC1213; M0ID:93077049
 A:Accession: PC1214
 A:Molecule type: mRNA
 A:Residues: 1-134 <HRN>
 A:Cross-References: GB:M98042; NID:9196749; PIDN:AAA8777.1; PID:9196750.
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-134/Product: Ig light chain V region #status predicted <MAT>
 F:36-116/Domain: immunoglobulin homology <IM>

Query Match 79.2%; Score 539.5; DB 2; Length 134;
 Best Local Similarity 78.9%; Pred. No. 5.2e-39;
 Matches 105; Conservative 14; Mismatches 13; Indels 1; Gaps 1;

QY 1 MDSQAQVLLILLMWSGTCGDIYLTQSPDSLAVSLGERATISCKSSQSLNSRTRENTLAWQ 60
 DB 1 MDSQAQVLLILLMWSGTCGDIYMSQSSSLTVSGEYVTKMCKSSQSLNSNMQNFIA 60
 QY 61 WYQKPGQPKLLIYASTRESGVPPDRFSGSGGTDTFTLTISLQAEVAVVYCTQSYNL 120
 DB 61 WYQKPGQPKLLIYASTRESGVPPDRFSGSGGTDTFTLTISVVAEDLAVVYCTQSYNL 120
 QY 121 -YTFGGTKEIK 132
 DB 121 PSYTFGGTKEIK 132

RESULT 9

S38807
 Ig light chain V-J region - mouse
 C:Species: Mus musculus (house mouse)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2001, 09:40:51 : Search time 15.22 Seconds
(without alignments)
297.091 Million cell updates/sec

Title: US-09-249-011-8
Perfect score: 681
Sequence: 1 MDSQAQVILLILLMWSCGTCG.....YCTOSYNLYTFGQGTKEIK 132

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 93435 seqs, 3425486 residues
Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	571.5	83.9	134	1	KV4C_HUMAN
2	552	81.1	133	1	KV4B_HUMAN
3	515	75.6	121	1	KV40_HUMAN
4	502.5	73.8	114	1	KV4A_HUMAN
5	446	65.5	129	1	KV3H_HUMAN
6	442	64.9	129	1	KV3L_HUMAN
7	440	64.6	129	1	KV3M_HUMAN
8	418	61.4	133	1	KV2E_HUMAN
9	416.5	61.2	129	1	KV1W_HUMAN
10	409.5	60.1	128	1	KV3K_HUMAN
11	408.5	60.0	131	1	KV3I_HUMAN
12	408.5	60.0	132	1	KV3F_MOUSE
13	396	58.1	115	1	KV3I_HUMAN
14	394.5	57.9	116	1	KV3J_HUMAN
15	394	57.8	110	1	KV3B_MOUSE
16	393.5	57.8	136	1	KV5B_MOUSE
17	392.5	57.6	149	1	KV5A_MOUSE
18	384	56.4	109	1	KV3E_HUMAN
19	384	56.4	109	1	KV3F_HUMAN
20	383	56.2	109	1	KV3D_HUMAN
21	382.5	56.2	111	1	KV3M_MOUSE
22	382.5	56.2	111	1	KV3O_MOUSE
23	381	55.9	109	1	KV3E_HUMAN
24	381	55.9	117	1	KV2E_HUMAN
25	380.5	55.9	108	1	KV3L_HUMAN
26	380.5	55.9	111	1	KV3L_MOUSE
27	379.5	55.7	111	1	KV3H_MOUSE
28	379.5	55.4	111	1	KV3H_MOUSE
29	375.5	55.1	111	1	KV3N_MOUSE
30	374.5	55.0	111	1	KV3O_MOUSE
31	374.5	55.0	111	1	KV3R_MOUSE
32	374.5	55.0	111	1	KV3S_MOUSE
33	373.5	54.8	115	1	KV2A_HUMAN

34	370	54.3	109	1	KV3G_HUMAN	P04206 homo sapien
35	368.5	54.1	117	1	KV1J_HUMAN	P01602 homo sapien
36	368.5	54.1	129	1	KV1X_HUMAN	P04432 homo sapien
37	367	53.9	108	1	KV3A_HUMAN	P01619 homo sapien
38	366.5	53.8	108	1	KV1V_HUMAN	P04430 homo sapien
39	366.5	53.8	111	1	KV3D_MOUSE	P03977 mus musculu
40	366.5	53.8	111	1	KV3J_MOUSE	P01662 mus musculu
41	366.5	53.8	111	1	KV3I_MOUSE	P01672 mus musculu
42	366.5	53.8	114	1	KV1A_MOUSE	P01632 mus musculu
43	365.5	53.7	108	1	KV1H_HUMAN	P01600 homo sapien
44	362.5	53.2	111	1	KV3C_MOUSE	P01656 mus musculu
45	362	53.2	113	1	KV2B_HUMAN	P01615 homo sapien

ALIGNMENTS

RESULT	1	STANDARD	PRT	134 AA.
KV4C_HUMAN				
ID	KV4C_HUMAN			
AC	P06314;			
DT	01-JAN-1988 (Rel. 06, Created)			
DT	01-APR-1988 (Rel. 07, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	IG KAPPA CHAIN V-IV REGION B17 PRECURSOR.			
OS	Homo sapiens (human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
NC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86041854; PubMed=2997713;			
RA	Marsh P., Mills F., Gould H.;			
RT	"Detection of a unique human V kappa IV germline gene by a cloned			
RL	cDNA probe."			
RN	Nucleic Acids Res. 13:6531-6544(1985).			
RP	REVISION TO 76.			
RA	Marsh P.;			
RL	Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
DR	EMBL: X02990; CNA26733.1; -			
DR	PIR: A01905; KAH017.			
DR	HSSP: P01789; ZMCP.			
DR	InterPro: IPR003006; -			
DR	Pfam: PF00047; Ig; 1.			
KW	Immunoglobulin V region; Signal.			
FT	STGNAL	1	20	
FT	CHAIN	21	134	
FT	DOMAIN	21	43	
FT	DOMAIN	21	60	
FT	DOMAIN	61	75	
FT	DOMAIN	76	82	
FT	DOMAIN	83	114	
FT	DOMAIN	115	121	
FT	DOMAIN	122	133	
FT	DISULEID	43	114	
FT	NON_TER	134	134	
SO	SEQUENCE	134 AA;	14966 MW;	6413A22PD0738832 CRC64;

Query Match 83.9%; Score 571.5; DB 1; Length 134;
Best Local Similarity 86.2%; Pred. No. 3,1e-52;
Matches 112; Conservative 6; Mismatches 11; Indels 1; Gaps 1;

OY	4	QAOVILLLWWSGTCGIVLTQSPDSLAVSLGERATITSCKSSQSGLNSRRENTLAWQ	63
Dd	4	QTOVFISILLMTSGAVGIWMQSPDSLAVSLGERATINCKSSQSGLTSSDKNKLAWQ	63
OY	64	QKPQGPPELLIYWASTRESGVPDFRSGSGSGCTDFTLTSSLOAEDEVAVYYCTQSYNL-VT	122
Dd	64	QKPQGPPELLIYWASTRESGVPDFRSGSGSGCTDFTLTSSLOAEDEVAVYYCOOYNLPWT	123
OY	123	FGQGKVEIK	132
Dd	124	FGQGKVEIK	133
<hr/>			
RESULT 2			
ID	KVAB_HUMAN	STANDARD:	PRT: 133 AA.
AC	P06313:		
DT	01-JAN-1988 (Rel. 06, Created)		
DT	01-JAN-1988 (Rel. 06, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	IG KAPPA CHAIN V-IV REGION JI PRECURSOR.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
OX	NCBI_Taxid=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEUJINE-86041853; PubMed-2997712;		
RA	Klobbeck H.G., Bornkamm G.W., Combrilato G., Mocikat R., Pohlenz H.D.,		
RA	Zachau H.G.;		
RT	"Subgroup IV of human immunoglobulin K light chains is encoded by a		
RT	single germ-line gene";		
RL	Nucleic Acids Res. 13:6515-6529(1985).		
CC	-----		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL: Z00022; CAA77317.1; .		
DR	PRT: A01904; KAHUTJ.		
DR	HSSP; P01789; ZMCP.		
DR	InterPro; IPR003006; .		
DR	Pfam; PF00047; 19; 1.		
KM	Immunoglobulin V region; signal.		
FT	SIGNAL	1	20
FT	CHAIN	21	133
FT	DOMAIN	21	43
FT	DOMAIN	44	60
FT	DOMAIN	61	75
FT	DOMAIN	76	82
FT	DOMAIN	83	114
FT	DOMAIN	115	122
FT	DOMAIN	123	132
FT	DISULFID	43	114
FT	NON_TER	133	133
SO	SEQUENCE	133 AA; 14632 MW; 5FB9353066744AF4 CNC64;	
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Query Match 81.1%; Score 552; DB 1; Length 133;			
Best Local Similarity 83.7%; Pred. No. 3.2e-50;			
Matches 108; Conservative 6; Mismatches 15; Indels 0; Gaps 0;			
OY	4	QAOVILLLWWSGTCGIVLTQSPDSLAVSLGERATITSCKSSQSGLNSRRENTLAWQ	63
Dd	4	QTOVFISILLMTSGAVGIWMQSPDSLAVSLGERATINCKSSQSGLTSSDKNKLAWQ	63
OY	64	QKPQGPPELLIYWASTRESGVPDFRSGSGSGCTDFTLTSSLOAEDEVAVYYCTQSYNL-VT	122
Dd	64	QKPQGPPELLIYWASTRESGVPDFRSGSGSGCTDFTLTSSLOAEDEVAVYYCOOYNLPWT	123
OY	123	FGQGKVEIK	132
Dd	124	FGQGKVEIK	133

ID	RESULT	AC	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ	BA	BB	BC	BD	BE	BF	BG	BH	BI	BJ	BK	BL	BM	BN	BO	BP	BQ	BR	BS	BT	BV	BW	BX	BY	BZ	CA	CB	CC	CD	CE	CF	CG	CH	CI	CJ	CK	CL	CM	CN	CO	CP	CQ	CR	CS	CT	CU	CV	CW	CX	CY	CZ	DA	DB	DC	DD	DE	DF	DG	DH	DI	DJ	DK	DL	DM	DN	DO	DP	DQ	DR	DS	DT	DU	DV	DW	DX	DY	DZ	EA	EB	EC	ED	EE	EF	EG	EH	EI	EJ	EK	EL	EM	EN	EO	EP	EQ	ER	ES	ET	EU	EV	EW	EX	EY	EZ	FA	FB	FC	FD	FE	FF	FG	FH	FI	FJ	FK	FL	FM	FN	FO	FP	FQ	FR	FS	FT	FU	FV	FW	FX	FY	FZ	GA	GB	GC	GD	GE	GF	GG	GH	GI	GJ	GK	GL	GM	GN	GO	GP	GQ	GR	GS	GT	GU	GV	GW	GX	GY	GZ	HA	HB	HC	HD	HE	HF	HG	HH	HI	HJ	HK	HL	HM	HN	HO	HP	HQ	HR	HS	HT	HU	HV	HW	HX	HY	HZ	IA	IB	IC	ID	IE	IF	IG	IH	II	IJ	IK	IL	IM	IN	IO	IP	IQ	IR	IS	IT	IU	IV	IV	IW	IX	IY	IZ	JA	JB	JC	JD	JE	JF	JG	JH	JI	JJ	JK	JL	JM	JN	JO	JP	JQ	JR	JS	JT	JU	JV	JW	JX	JY	JZ	KA	KB	KC	KD	KE	KF	KG	KH	KI	KJ	KK	KL	KM	KN	KO	KP	KQ	KR	KS	KT	KU	KV	KW	KX	KY	KZ	LA	LB	LC	LD	LE	LF	LG	LH	LI	LJ	LK	LL	LM	LN	LO	LP	LQ	LR	LS	LT	LU	LV	LW	LX	LY	LZ	MA	MB	MC	MD	ME	MF	MG	MH	MI	MJ	MK	ML	MM	MN	MO	MP	MQ	MR	MS	MT	MU	MV	MW	MX	MY	MZ	NA	NB	NC	ND	NE	NF	NG	NH	NI	NJ	NK	NL	NM	NO	NP	NQ	NR	NS	NT	NU	NV	NW	NX	NY	NZ	OA	OB	OC	OD	OE	OF	OG	OH	OI	OJ	OK	OL	OM	ON	OO	OP	OQ	OR	OS	OT	OU	OV	OW	OX	OY	OZ	PA	PB	PC	PD	PE	PF	PG	PH	PI	PJ	PK	PL	PM	PN	PO	PP	PQ	PR	PS	PT	PV	PW	PX	PY	PZ	QA	QB	QC	QD	QE	QF	QG	QH	QI	QJ	QK	QL	QM	QN	QO	QP	QQ	QR	QS	QT	QU	QV	QW	QX	QY	QZ	RA	RB	RC	RD	RE	RF	RG	RH	RI	RJ	RK	RL	RM	RN	RO	RP	RQ	RR	RS	RT	RU	RV	RW	RX	RY	RZ	SA	SB	SC	SD	SE	SF	SG	SH	SI	SJ	SK	SL	SM	SN	SO	SP	SQ	SR	SS	ST	SV	SW	SX	SY	SZ	TA	TB	TC	TD	TE	TF	TG	TH	TI	TJ	TK	TL	TM	TN	TO	TP	TQ	TR	TS	TT	TU	TV	TW	TX	TY	TZ	UA	UB	UC	UD	UE	UF	UG	UH	UI	UJ	UK	UL	UM	UN	UO	UP	UQ	UR	US	UT	UU	UV	UW	UX	UY	UZ	VA	VB	VC	VD	VE	VF	VG	VH	VI	VJ	VK	VL	VM	VN	VO	VP	VQ	VR	VS	VT	VU	VV	VX	VY	VZ	WA	WB	WC	WD	WE	WF	WG	WH	WI	WJ	WK	WL	WM	WN	WO	WP	WQ	WR	WS	WT	WU	WV	WW	WX	WY	WZ	XA	XB	XC	XD	XE	XF	YG	YH	YI	YJ	YK	YL	YM	YN	YO	YP	YQ	YR	YS	YT	YU	YV	YW	YX	YY	YZ	ZA	ZB	ZC	ZD	ZE	ZF	ZG	ZH	ZI	ZJ	ZK	ZL	ZM	ZN	ZO	ZP	ZQ	ZR	ZS	ZT	ZU	ZV	ZW	ZX	ZY	ZZ
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DR 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-IV REGION LEN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76004342; PubMed=50995;
RA Schneider M., Hilschmann N.;
RT "The primary structure of a monoclonic immunoglobulin-L-chain of
RT subgroup IV of the kappa type (Bence-Jones protein len.).";
RL Hope-Seyler's 2. Physiol. Chem. 356:507-557(1975).
RN [2]
RP REVISION TO 9.
RA Salomon A.;
RL Submitted (AUG-1996) to the SWISS-PROT data bank.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01903; KAHUIN.
DR HSSP: P01789; 2MCP.
DR InterPro: IPR003006;
DR Pfam: PF00047; 19; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 41 55 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 56 62 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 4 63 94 FRAMEWORK 3.
FT DOMAIN 5 95 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 6 102 113 FRAMEWORK 4.
FT DISULFID 23 94 BY SIMILARITY.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;

Query Match 73.8%; Score 502.5; DB 1; Length 114;
Best Local Similarity 86.7%; Pred. No. 3.4e-45;
Matches 98; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

OY 21 DIVTQSPDLAVSLGERATISCKSSQSLNSTRRENYLAWYQKRGQPKLLIYASTR 80
DB 1 DIVTQSPDLAVSLGERATINCKSSQSVLYSSNSKNYLAWYQKRGQPKLLIYASTR 60
OY 81 ESGVDPFSGSGSGTFTLTISLQAEADVAVYCTOSYNL-YFPGGCTKVEIK 132
DB 61 ESGVDPFSGSGSGTFTLTISLQAEADVAVYCTOSYNL-YFPGGCTKLEIK 113

RESULT 5
KV3L_HUMAN STANDARD; PRT; 129 AA.
ID P04207;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION CLL PRECURSOR (RHEUMATOID FACTOR).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86177570; PubMed=3083417;
RA Jirik F.R., Sorge J., Fong S., Heltmann J.G., Cud J.G., Chen P.P.,
RA Goldfien R., Carson D.A.;
RT "Cloning and sequence determination of a human rheumatoid factor
RT light-chain gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
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CC -----
DR EMBL: M12740; AAA58992.1; -
DR PIR: A01898; K3HUGL.
DR HSSP: P01789; 2MCP.
DR InterPro: IPR003006;
DR Pfam: PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION CLL.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 2 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 55 69 FRAMEWORK 2.
FT DOMAIN 4 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 77 108 FRAMEWORK 3.
FT DOMAIN 6 109 118 FRAMEWORK 3.
FT DOMAIN 7 119 129 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 108 UKI SEGMENT.
FT NON_TER 129 129 BY SIMILARITY.
SQ SEQUENCE 129 AA; 14275 MW; 5C13BA11BE60CC14 CRC64;

Query Match 65.5%; Score 446; DB 1; Length 129;
Best Local Similarity 66.7%; Pred. No. 2.7e-39;
Matches 90; Conservative 20; Mismatches 15; Indels 10; Gaps 3;

OY 1 MDSQAVLLILLVSGTSDIVLTQSPDSLAVSLGERATISCKSSQSLNSTRRENYLA 60
DB 1 MEAPQQLILLMLPDTTGEIVMTQSPATLSPGERATLSCRASQSVNN-----LA 54
OY 61 WYQKRGQPKLLIYASTRESGVDPFSGSGSGTFTLTISLQAEADVAVYCTOSYN- 119
DB 55 WYQKRGQPKLLIYASTRGATIGPARFSGSGSGTFTLTISLQAEADVAVYCT- 113
OY 120 --LYTFGGCTKVEIK 132
DB 114 WPMTEFGGCTKVEIK 128

RESULT 6
KV3L_HUMAN STANDARD; PRT; 129 AA.
ID P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION HAH PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Antenatally-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR: P10022; K3HUGA.
DR HSSP: P01789; 2MCP.
DR InterPro: IPR003006;
DR Pfam: PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.

```

FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 56 70 FRAMEWORK 2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JKI SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14073 MM; D3C55292772774D0 CRC64;

Query Match 64.9%; Score 442; DB 1; Length 129;
Best Local Similarity 66.9%; Pred. No. 7e-39;
Matches 89; Conservative 19; Mismatches 19; Indels 6; Gaps 2;

OY 1 MDSQAQVILLILLWVSGCGDIVLTQSPDSLAVSLGERATISCKSSQSLNSRRENTLYA 60
DB 1 METPQAQLFLILLWLPDPTTGEIVLTQSPGTLISLSPGERATISCRASQSVSSS-----YLA 55
OY 61 WYQKPGQPKLLIYMASTRRESGVDPDRFSGSGSGTDFTLTISLSLAEDVAVYYCTQ-SYN 119
DB 56 WYQKPGQAPRLIIYGASSRATGIPDRFSGSGSGTDFTLTISRLPEDPFAYVYCCQYQTS 115
OY 120 LYTFGQGTKEIK 132
DB 116 PRTFGQGTKEIK 128

RESULT 7
KV3M_HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION HIC PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
CC PIR: PU0021; K3HUH1.
DR HSSP: P01789; 2MCP.
DR InterPro: IPR003006; -
DR Pfam: PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 21 129 IG KAPPA CHAIN V-II REGION HIC.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 56 70 FRAMEWORK 2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JKI SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14070 MM; 7395528EA2BB74D6 CRC64;

Query Match 64.6%; Score 440; DB 1; Length 129;
Best Local Similarity 66.2%; Pred. No. 1.1e-38;

Matches 88; Conservative 20; Mismatches 19; Indels 6; Gaps 2;

OY 1 MDSQAQVILLILLWVSGCGDIVLTQSPDSLAVSLGERATISCKSSQSLNSRRENTLYA 60
DB 1 METPQAQLFLILLWLPDPTTGEIVLTQSPGTLISLSPGERATISCRASQSVSSS-----YLA 55
OY 61 WYQKPGQPKLLIYMASTRRESGVDPDRFSGSGSGTDFTLTISLSLAEDVAVYYCTQ-SYN 119
DB 56 WYQKPGQAPRLIIYGASSRATGIPDRFSGSGSGTDFTLTISRLPEDPFAYVYCCQYQTS 115
OY 120 LYTFGQGTKEIK 132
DB 116 PRTFGQGTKEIK 128

RESULT 8
KV2E_HUMAN STANDARD; PRT; 133 AA.
AC P06310;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION RPMI 6410 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobbeck H.G., Meinl A., Combriato G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
RT III.";
RL Nucleic Acids Res. 13:6499-6513(1985).
CC -----
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CC -----
CC EMBL: Z00020; CAAT7315.1; -
DR PIR: A01890; K2HURP.
DR InterPro: IPR003006; -
DR Pfam: PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 21 133 IG KAPPA CHAIN V-II REGION RPMI 6410.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 59 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 60 74 FRAMEWORK 2.
FT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 82 113 FRAMEWORK 3.
FT DOMAIN 114 122 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 123 132 FRAMEWORK 4.
FT DISULFID 43 113 BY SIMILARITY.
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14707 MM; 513CCA3F3673009EE CRC64;

Query Match 61.4%; Score 418; DB 1; Length 133;
Best Local Similarity 65.9%; Pred. No. 2.2e-36;
Matches 85; Conservative 19; Mismatches 23; Indels 2; Gaps 2;

OY 5 AQLGLILLWVSGCGDIVLTQSPDSLAVSLGERATISCKSSQSLNSRRENTLYA 64
DB 5 AQLGLILLWVSGCGDIVLTQSPDSLAVSLGERATISCKSSQSLNSRRENTLYA 64
OY 65 KPGQPKLLIYMASTRRESGVDPDRFSGSGSGTDFTLTISLSLAEDVAVYYCTQ-SYN 123
DB 64 KPGQPKLLIYMASTRRESGVDPDRFSGSGSGTDFTLTISLSLAEDVAVYYCTQ-SYN 123

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ID      KV3K_HUMAN          STANDARD;       PRT;       128 AA.
AC      P06311:
DT      01-JAN-1988 (Rel. 06, Created)
DT      01-JAN-1988 (Rel. 06, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      IG KAPPA CHAIN V-II REGION IARC/BL41 PRECURSOR.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC      Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
CX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=86041852; PubMed=2997711;
RA      Klobbeck H.G., Meindl A., Combiatico G., Solomon A., Zachau H.G.;
RT      "Human immunoglobulin kappa light chain genes of subgroups II and
RT      III."
RL      Nucleic Acids Res. 13:6499-6513(1985).
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@sib-sib.ch).
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DR      EMBL; 200021; CAA77316.1; -.
DR      PIR; A01899; K3H041.
DR      InterPro; IPRO03006; -.
DR      Pfam; PF00047; Ig; 1.
KW      Immunoglobulin v region; Signal.
FT      SIGNAL             1     20
FT      CHAIN              1     128
FT      DOMAIN             21     43   IG KAPPA CHAIN V-II REGION IARC/BL41.
FT      DOMAIN             44     54   FRAMEWORK 1.
FT      DOMAIN             55     69   COMPLEMENTARITY-DETERMINING 1.
FT      DOMAIN             70     76   FRAMEWORK 2.
FT      DOMAIN             77     108  COMPLEMENTARITY-DETERMINING 2.
FT      DOMAIN            109    117   FRAMEWORK 3.
FT      DOMAIN            118    128   COMPLEMENTARITY-DETERMINING 3.
FT      DISULFID           43     108  JK1 SEGMENT.
FT      NON_TER            128    128  BY SIMILARITY.
SO      SEQUENCE          128 AA; 14070 MW; CC8957F0EE3B9012 CRC64;.

Query Match               60.1%; Score 409.5; DB 1; Length 128;
Best Local Similarity     63.2%; Pred. No. 1,6e-35;
Matches 84; Conservative 21; Mismatches 21; Indels 7; Gaps 2.

QY      1 MDSQAQVILLLLWVSGTGCDIVLTQSPDSLAVSLGERATISKSSQSILNSRRENYLA 60
        ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      1 METPAQLFLLLLMVDPDTGGEIVLTQSPGTLSLSPGESATLSCRASQSVSN-----LA 54

QY      61 WYQQKPGQPKPLIYWASTRESGVDRSRSGSSGGDFITLTISLDAEDYAIVYCQO-SIN 119
        :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      55 WYQQKRGSGPRLLIRDASRANGIPDRFGSGSGDFTLISRLEPEDFAVVYCOYSYS 114

QY      120 LYTFGGTKRKVEIK 132
        |||||||::|::|
DB      115 PTTFGGTKLKLEIK 127

RESULT  11
KV3J_MOUSE
ID      KV3J_MOUSE          STANDARD;       PRT;       131 AA.
AC      P01661;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      IG KAPPA CHAIN V-II REGION MOPC 63 PRECURSOR.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC      Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN
RP SEQUENCE OF 1-35.
RX MEDLINE=78235887; PubMed=98179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled
RT expression of immunoglobulin genes.";
RL Biochemistry 17:2392-2400(1978).
RN
RP SEQUENCE OF 21-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKeon D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences.";
RL Biochemistry 12:760-771(1973).
RN
RP REVISIONS.
RX MEDLINE=79012520; PubMed=99744;
RA McKeon D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
DR PIR: A01935; KWSM6.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; 1g: 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 131 IG KAPPA CHAIN V-III REGION MOPC 63.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 59 73 FRAMEWORK 2.
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 81 112 FRAMEWORK 3.
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 122 131 FRAMEWORK 4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;

Query Match 60.0%; Score 408.5; DB 1; Length 131;
Best Local Similarity 62.4%; Pred. No. 2e-35;
Matches 83; Conservative 21; Mismatches 26; Indels 3; Gaps 2;

OY 1 MDSQAVLILLWVSGTGDIVLTQSPDSLAVSGERATISCKSSQSLNSRTRENTLA 60
DB 1 METDILLWVLLWVPGSTGIVLTQSPASLAVSLGQRATISCRASESV--DSYGNSTFMH 58
OY 61 WYQKPGQPKLLIYMASTRESGVPDRFGSGSGTDFTLTISLQAEDVAVYYCTQ--SYN 119
DB 59 WYQKPGQPKLLIYLAENLSEGVAPRFGSGSGSRDFTLTIDPVADDAATFYCCQNNED 118
OY 120 LTFEGSGTKVEIK 132
DB 119 PWTEGGGTKLEIK 131

RESULT 12
KV3F_MOUSE STANDARD: PRT; 132 AA.
ID KV3F_MOUSE
AC P04553;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION MOPC 321 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-37.

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RX MEDLINE=78235887; PubMed=98179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled
RT expression of immunoglobulin genes.";
RL Biochemistry 17:2392-2400(1978).
RN
RP SEQUENCE OF 21-132.
RX MEDLINE=73140224; PubMed=4120629;
RA McKeon D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Partial amino acid sequence of a kappa
RT chain.";
RL Biochemistry 12:749-759(1973).
CC -1 MISCELLANEOUS: "THE PARTIAL SEQUENCE OF THE C REGION OF THIS
CC BENCE-JONES PROTEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT
CC REPORTED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY
CC RESIDUES."
DR PIR: A01933; KWS32.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; 1g: 1.
KW Immunoglobulin V region; Bence-Jones protein; Signal.
FT SIGNAL 1 20
FT CHAIN 21 132 IG KAPPA CHAIN V-III REGION MOPC 321.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 59 73 FRAMEWORK 2.
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 81 112 FRAMEWORK 3.
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 122 131 FRAMEWORK 4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON_TER 132 132
SQ SEQUENCE 132 AA; 14523 MW; 9F3B809BB773FBE9 CRC64;

Query Match 60.0%; Score 408.5; DB 1; Length 132;
Best Local Similarity 58.6%; Pred. No. 2.1e-35;
Matches 78; Conservative 28; Mismatches 24; Indels 3; Gaps 2;

OY 1 MDSQAVLILLWVSGTGDIVLTQSPDSLAVSGERATISCKSSQSLNSRTRENTLA 60
DB 1 METDILLWVLLWVPGSTGIVLTQSPASLAVSLGQRATISCRASKSV--NTYGNSTFMZ 58
OY 61 WYQKPGQPKLLIYMASTRESGVPDRFGSGSGTDFTLTISLQAEDVAVYYCTQS--YN 119
DB 59 WYZZKPGQPKLLIYRAENLSEGVAPRFGSGSGSRDFTLTIDPVZABDVATFYCCZSSBZ 118
OY 120 LTFEGSGTKVEIK 132
DB 119 PWTEGGGTKLEIK 131

RESULT 13
KV3I_HUMAN STANDARD: PRT; 115 AA.
ID KV3I_HUMAN
AC P04433;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION VG PRECURSOR (FRAMEWORK).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
RT within the YK locus";
RL Nucleic Acids Res. 12:9229-9236(1984).
CC -----

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Query Match	58.18;	Score 396;	DB 1;	Length 115;
Best Local Similarity	65.58;	Pred. No. 3.4e-34;		
Matches 78; Conservative	17;	Mismatches 18;	Indels 6;	Gaps 1;

RESULT	14
KV3J_HUMAN	
ID	KV3J_HUMAN
STANDARD;	
PRT;	116 AA

Immunoglobulin V region; Signal

Query Match	57.9%;	Score 394.5;	DB 1;	Length 116;
Best Local Similarity	64.2%;	Pred. No. 4.9e-34;		
Matches 77; Conservative	18;	Mismatches 20;	Indels 5;	Gaps 1

RESULT	15
KV3P_MOUSE	
ID_KV3P_MOUSE	STANDARD;
	PRT; 110 AA

RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin

Query Match	57.9%;	Score 394;	DB 1;	Length 110;
Best Local Similarity	70.5%;	Pred. No. 5.2e-34;		
Matches	79;	Conservative	11;	Mismatches 20;
			Indels	2;
			Gaps	1

59 ESCIPARFSGSGCTDTLNIHPVEEDATYCHQSEDPTWFGSGTKLEIK 110

Mon Apr 30 07:08:35 2001

us-09-249-011-8.rsp

Page 8

Search completed: April 25, 2001, 09:40:51
Job time: 176 sec

Query Match	55.7%	Score 379.5	DB 4	Length 108
Best Local Similarity	66.4%	Pred. No. 4	1e-33	
Matches	75	Conservative	15	Mismatches 16
				Indels 7
				Gaps 2

RESULT	3	
09UL78		
ID	09UL78	PRELIMINARY;
AC	09UL78;	PRT; 109 AA.
DT	01-MAY-2000 (TREMBLrel. 13, Created)	
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)	
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eultheria; Primates; Carnivora; Homiidae; Homo.	
OX	NCBI_TaxID=9606;	

RN	111			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98277139; PubMed=9614934;			
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,			
RA	Young D.C.;			
RT	"Yosin-reactive autoantibodies in rheumatic carditis and normal			
RT	fetus.";			
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).			
DR	EMBL: AF035036; AAD56272.1; -.			
DR	HSSP; P01789; IMCP.			
DR	INTERPRO: IPR003006; -.			
DR	PFAM: PF00047; Ig; 1.			
ET	NON_TER	1	1	
ET	NON_TER	109	109	
SO	SEQUENCE	109 AA;	11646 MW;	56675C52EC7BE197 CRC64;

Query Match 55.7%; Score 379; DB 4; Length 109;
Best Local Similarity 68.1%; Pred. No. 4.7e-33.

RESULT	4
090UL79	
ID 090UL79	
090UL79:	PRELIMINARY; PRT: 108 AA.

RN
 (11)
 RP
 SEQUENCE FROM N.A.
 RX
 MEDLINE=98271139; PubMed=9614934;
 RA
 Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 Young D.C.;
 TWOST-1-reactive autoantibodies in rheumatic carditis and normal

Query Match	55.1%	Score 375.5	DB 4	Length 108
Best Local Similarity	67.3%	Pred. No. 1.1e-32		
Matches 76	Conservative 11	Mismatches 19	Indels 7	Gaps 2

QY	21	DIYLTQSPDLSLAVSLGERATISCKSSOSILNSTRRENTYLANVYQKPGCPKLLIYMASTR	80
	1	DIYVMTQSPSLLSASTGDRVTISCRMSQCI-----SSYLANVYQKPGKAPPELLIYAASTL	54
QY	81	ESGVPRDFRSGSGSTDFLTITSSLSQAEVDVAYYCTQSNL--YTQCGTKRVEIK	132
Db	55	QSGVPSRPSGSGSTDFLTITSSLSQAEVDVAYYCOOYISFPPTQGRKVEIK	107
RESULT	5		

ID	OSUL70	PRELIMINARY:	PRT:	108 AA.
AC	OSUL70;			
DT	01-MAY-2000 (TREMBLrel.13, Created)			
DT	01-MAY-2000 (TREMBLrel.13, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel.15, Last annotation update)			
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98277139; PubMed=9614934;			
WA	Wu X., Liu B., Van der Merwe P.L., Kals N.N., Berney S.M.,			

RT	RA
RT	Young D. C.;
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).


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RESULT 9
Q9UL80 ID 09UL80 PRELIMINARY: PRT: 114 AA.
AC 09UL80:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
DR Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035034; AAD56270.1; -.
DR INTERPRO: IPR003006; -.
DR PIRAM: PF00047; 19; 1.
FT NON_TER 1 1
FT NON_TER 114 114
SO SEQUENCE 114 AA; 12775 MW; 070E31E210DICB01 CRC64;

Query Match
Best Local Similarity 51.8%; Score 352.5; DB 4; Length 114;
Matches 73; Conservative 15; Mismatches 23; Indels 3; Gaps 2;

Db 21 DIVLQSPDLSLAVSGERATISCKSSQSLNSRTRENYLAWYQOKPGQPKLLIYMASTR 80
1 DVMTQSLSLPVLTKROKASISCKSSQSPVYS-DCNTILNMFQOKRPPRLIYKVSNR 59
QY 81 EGVGPDREFSGSGGTDTLTITSSLOAEDVAVYCTQS--YVLYTFGGCTKVEIK 132
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 DSGVDRFSGSGGTDTLTITSSLOAEDVAVYCTQSGTGMWPMWTFGGCTKVEIK 113

RESULT 10
Q9JL82 ID 09JL82 PRELIMINARY: PRT: 104 AA.
AC 09JL82:
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF206024; AAF69322.1; -.
FT NON_TER 1 1
FT NON_TER 104 104
SO SEQUENCE 104 AA; 11360 MW; 5DA8BBF05FOAIAAE CRC64;

Query Match
Best Local Similarity 50.1%; Score 341; DB 11; Length 104;
Matches 69; Conservative 16; Mismatches 17; Indels 2; Gaps 2;

QY 30 SLAVSLGERATISCKSSQSLNSRTRENYLAWYQOKPGQPKLLIYMASTRSGVDPDRFS 89
```

```
Db 2 SLVPSLGDQASISCKSSQSLVHT-NGNTYLMHYLQKPGQSPKLLIYKVSNRSGVDPDRFS 60
QY 90 GSGSGTDTLTITSSLOAEDVAVYCTQSYNL-YTFGGCTKVEIK 132
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GSGSGTDTLTITSSLOAEDVAVYCTQSYTHVPTTFGGCTKVEIK 104

RESULT 11
Q9JL74 ID 09JL74 PRELIMINARY: PRT: 99 AA.
AC 09JL74:
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF206032; AAF69330.1; -.
FT NON_TER 1 1
FT NON_TER 99 99
SO SEQUENCE 99 AA; 10939 MW; 3B25D0E7B453324 CRC64;

Query Match
Best Local Similarity 49.4%; Score 336.5; DB 11; Length 99;
Matches 67; Conservative 14; Mismatches 15; Indels 7; Gaps 2;

Db 31 LAVSLGERATISCKSSQSLNSRTRENYLAWYQOKPGQPKLLIYMASTRSGVDPDRFS 90
1 LLSVSGDRVTITCKAKSQSVSD-----VAVYQOKPGQSPKLLIYASNRITGVDPDRFG 56
QY 91 SSGSGTDTLTITSSLOAEDVAVYCTQSYNL-YTFGGCTKVEIK 132
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 57 SSGSGTDTLTITSSLOAEDVAVYCTQSDYSSPRTGGCTKVEIK 99

RESULT 12
Q9RIAS ID 09RIAS PRELIMINARY: PRT: 214 AA.
AC 09RIAS:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
DE KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Mitra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv)."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF152371; AAD40242.1; -.
DR HSSP: P01789; IMCP.
DR INTERPRO: IPR003006; -.
DR PIRAM: PF00047; 19; 2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1 1
FT NON_TER 214 214
SO SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;
```


Search completed: April 25, 2001, 09:40:34
Job time: 199 sec

PN WO200047625-A2.

PD 17-AUG-2000.

PF 09-FEB-2000; 2000WO-US03303.

PR 12-FEB-1999; 99US-0249011.

PR 24-JUN-1999; 99US-0339596.

PX (GEMV) GENETICS INST INC.

PA

PI Co MS, Vasquez M, Carreno B, Celnikier AC, Collins M, Goldman S;

PI Gray GS, Knight A, O'hara D, Rup B, Veldman GW;

XX N-PSDB; A59695.

DR WPI: 2000-524532/47.

PT Humanized immunoglobulin having a binding specificity to B7-1 (derived from ATCC PTA-263), or B7-2 (derived from ATCC CRL-1524) molecules, modulates immune responses and can therefore treat e.g. autoimmune diseases, infectious diseases -

PT

PS Example 3; Fig 2B; 162pp: English.

XX

XX The present sequence represents the light chain variable region of the humanised murine antibody 3D1. The antibody has a binding specificity to B7 molecules. The antibody is used to construct humanized immunoglobulins, which comprise an antigen binding region of non-human origin and a portion of a human immunoglobulin. The humanized immunoglobulins are useful for treating autoimmune diseases, infectious diseases, inflammatory disorders, systemic lupus erythematosus, diabetes mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease, inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are also useful for treating a transplant recipient and preventing transplant rejection in a transplant recipient, and treating proliferative disease (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia, thalassemia and aplastic anaemia), Inborn errors of metabolism, congenital immunodeficiency diseases, and myeloid dysplasia syndrome.

CC

CC Sequence 132 AA:

SQ

Query Match 100.0%; Score 681; DB 21; Length 132;
Best Local Similarity 100.0%; Pred. NO. 3.5e-47;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDQAQAVLLILLMWSCGTGLIVLPQSPSLAWLGEARATISCKSSQSILNSRTRENYLA 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 mdsqgqvlllllllwwsgtcdilvltqpsdlsavslgeratlscskssqslinstrenyla 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 61 WYQKRGPPKLIIWASTRESGVDPDRFSGSGSDTFTLTISLSLOAEVAAYYYCTQSYNL 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 wyqkrgppgpklllywastresgvdpdrfsgsgsdftltltslsgdeavayyctqsyln 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 121 YTFGGGTKEIK 132
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 ytfgggtkveik 132

RESULT 2
ID B07964
AC B07964 standard; Protein: 132 AA.
XX
XX 14-NOV-2000 (first entry)
DE Amino acid sequence of light chain variable region of 3S1 antibody.
KW Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;
KW autoimmune disease; Infectious disease; inflammatory disorder;
KW systemic lupus erythematosus; diabetes mellitus; insulinitis; asthma;
KW arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;

KW		multipliclerosis; transplant rejection; proliferative disease;
KW		leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
KW		aplastic anaemia; myeloid dysplasia syndrome.
OS	Mus sp.	
FH	Key	Location/Qualifiers
FT	Peptide	1..20
FT		/note= "signal peptide"
FT	Protein	21..132
FT		/note= "mature protein"
FT	Region	44..60
FT		/note= "complementarity determining region 1"
FT	Region	76..82
FT		/note= "complementarity determining region 2"
FT	Region	115..122
FT		/note= "complementarity determining region 3"
PN	WO20047625-A2.	
PD	17-AUG-2000.	
XX		
PP	09-FEB-2000; 2000WO-US03303.	
PR	12-FEB-1999; 99US-0249011.	
PR	24-JUN-1999; 99US-0339596.	
PA	(GENEX) GENETICS INST INC.	
XI	Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S,	
PI	Gray GS, Knight A, O'hara D, Rup B, Veldman GM.	
XX		
DR	WPI: 2000-524532/47	
XX	N-PSTDB: A59693.	
PT	Humanized immunoglobulin having a binding specificity to B7-1 (derived from ATCC PTA-263), or B7-2 (derived from ATCC CRL-1524) molecules, modulates immune responses and can therefore treat e.g. autoimmune diseases, infectious diseases -	
PS	Example 1; Fig 1B; 162pp; English.	
CC	The present sequence represents the light chain variable region of the murine antibody 3D1. The antibody has a binding specificity to B7 molecules. The antibody is used to construct humanized immunoglobulins, which comprises an antigen binding region of non-human origin and a portion of a human immunoglobulin. The humanized immunoglobulins are useful for treating autoimmune diseases, infectious diseases, inflammatory disorders, systemic lupus erythematosus, diabetes mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease, CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are also useful for treating a transplant recipient or preventing transplant rejection in a transplant patient, and treating proliferative disease (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia, thalassemia and aplastic anaemia), inborn errors of metabolism, congenital immunodeficiency diseases, and myeloid dysplasia syndrome.	
SQ	Sequence 132 AA:	
OY	Query Match 92.4%; Score 629; DB 21; Length 132; Best Local Similarity 90.9%; Pred. No. 4.6e-43;	
DG	Matches 120; Conservative 7; Mismatches 5; Indels 0; Gaps 0;	
OY	1 MDQAQVILLILAWSGTGCDIVLTQSPSLAVLGERATISKSSQSLLSRTRENYLA 60 1 mdsqgqvlllilwsgtgcdivltqspslavsaagekymsckssqslnrtrenyla 60	
OY	61 WYQGKPGCPKKLIYWASTRESGVDPDRSRGSGETDTITISLDAEDVAAYVCQTGYNL 120 61 wyqkpgspskliywastresgvdpdrifgsqgdftitissvaeadvayvcqtgsynl 120	
OY	121 YTFGGTKEIK 132	

Db 121 ytfgggtkleik 132

RESULT 3

P93078 standard; peptide: 148 AA.

P93078;

14-MAR-1990 (first entry)

Light chain of monoclonal antibody 6A4.

Monoclonal antibody 6A4; light chain; Pseudomonas aeruginosa; OMP-1.

EP338395-A.

25-OCT-1989.

12-APR-1989; 89EP-0106463.

19-APR-1988; 88DE-3813023.

(BEHM) BEHRINGWERKE.

Domdey H, Marget M, von Specht BU;

WPI; 1989-310861/43.

N-PSDB; N91663.

Monoclonal antibody to Pseudomonas aeruginosa and DNA coding for variable antibody regions.

Claim 1; page 6; 7pp; german.

The peptide is encoded by the light chain of monoclonal antibody 6A4.

6A4 reacts with the OMP-1 protein of all 19 known serotypes of P.aeruginosa. It is used for therapy and diagnosis of infection, and as a carrier for drugs. The antibody is IgG2a subclass.

Sequence 148 AA;

Query Match 87.5%; Score 596; DB 10; Length 148;

Best Local Similarity 86.4%; Pred. No. 2.1e-40; Mismatches 8; Indels 0; Gaps 0;

Matches 114; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 1 MDSQAOVLILLVMSGTCGDIYLTQSPDSLAVSLGERATISCKSSQSLNSRTRENYLA 60
 Db 1 mdsqagvlllllllwsqtcgdilwmsqpslavsagekvmsckssqslinslrknfla 60
 QY 61 WYQOKFGQPKLLIYMASTRSGVDPDRFSGSGGTFDTLTISLQAEVAVYCTOSYNL 120
 Db 61 wygqkpgspklllywastresgvdpdrftlsgsgtdftlissvgaedlavyyckqsyln 120
 QY 121 YTFGQGTKEIK 132
 Db 121 rtfgggtkleik 132

RESULT 4

R76087 standard; Protein: 239 AA.

R76087;

21-NOV-1995 (first entry)

MAB 55.1 light chain.

Antigen binding structure; complementarity determining region; CDR;

CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;

KW monoclonal antibody; MAB; immunotherapy; therapy; diagnosis;
 KW transgenic animal; transgenic plant; antibody engineering;
 KW humanized antibody; immunotoxin.

Mus sp.

Key Location/Qualifiers

Peptide 1..20

Protein /label= Sig_peptide

FT 21..239

FT /label= Mat_protein

FT /note= "claim 3, page 98"

WO9515382-A.

08-JUN-1995.

29-NOV-1994; 94WO-GB02610.

03-JUN-1994; 94GB-0011089.

03-DEC-1993; 93GB-0024819.

(ZENEC) ZENECAL LTD.

Blakey DC, Boot C, Copley CG, Hall SM, Paterson DS;

Rose MS, Wright AF;

WPI; 1995-215262/28.

N-PSDB; Q94036.

Antigen binding structures containing CDRs recognising the CA55.1 antigen - produced by hybridomas and host cells, for use in the diagnosis and therapy of cancer

Disclosure; Fig.16; 121pp; English.

MAB 55.1 (ECACC 93081901) recognises the colorectal tumor-associated

CC chains of 55.1. cDNAs for the heavy (Q94037) and light (Q94036)

CC chains of 55.1 were isolated, and F(ab)', F(ab)2, Fab, Fv, scfv or

CC v-m in humanized 55.1 constructs have been expressed in myeloma

CC cells and E. coli.

Sequence 239 AA;

Query Match 86.9%; Score 592; DB 16; Length 239;
 Best Local Similarity 84.8%; Pred. No. 7e-40; Mismatches 9; Indels 0; Gaps 0;
 Matches 112; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 MDSQAOVLILLVMSGTCGDIYLTQSPDSLAVSLGERATISCKSSQSLNSRTRENYLA 60
 Db 1 mdsqagvlllllllwsqtcgdilwmsqpslavsagekvmsckssqslinslrknfla 60
 QY 61 WYQOKFGQPKLLIYMASTRSGVDPDRFSGSGGTFDTLTISLQAEVAVYCTOSYNL 120
 Db 61 wygqkpgspklllywastresgvdpdrftlsgsgtdftlissvgaedlavyyckqsyln 120
 QY 121 YTFGQGTKEIK 132
 Db 121 rtfgggtkleik 132

RESULT 5

W10545 standard; Protein: 137 AA.

W10545;

25-SEP-1997 (first entry)

Humanised murine anti-E-selectin antibody Cy1788V(LB).

Humanised; murine; mouse; E-selectin; antibody; light chain;

```
KW variable region; detection; inhibition; mediation; cell adhesion;  
KW diagnosis: reduction; inflammation; septic shock; ARDS; sepsis;  
KM acute respiratory distress syndrome; gross cystic breast disease;  
KM cancer treatment; splanchnic occlusion shock; psoriasis;  
XX complement; chimeric.  
OS Chimeric - Mus spp.  
OS Chimeric -- Homo sapiens.  
OS Synthetic.  
XX  
PN W09640942-AI.  
PD 19-DEC-1996.  
XX  
PF 06-JUN-1996;. 96WO-US09204.  
PR 07-JUN-1995;. 95US-0482112.  
PA (CYTE-) CYTEL CORP.  
PI Bendig MM, Jones ST, Perez C, Saldanha JW, Williams MA,  
PJ Jones S;  
XX  
DR MPI: 1997-077272/07.  
N-PSDB: T60730.  
XX  
PT Humanised anti-E-selectin antibody - useful for diagnosis and  
pr treatment of, e.g., inflammatory responses, septic shock, acute  
respiratory distress syndrome or cancer  
XX  
PS Claim 18; Page 71; 89pp; English.
```

The present sequence is the humanised murine anti-E-selectin antibody (Ab) light chain variable region, CY1788V(LB). The Ab can be used to detect E-selectin, or inhibit E-selectin mediated cell adhesion. It can also be used to diagnose, reduce or inhibit an inflammatory response, or the severity of pathologies, e.g. septic shock, acute respiratory distress syndrome, wound associated CC sepsis, gross cystic breast disease or cancer, or treat, e.g. splanchnic occlusion shock, or psoriasis. It can be administered to CC a human without inducing an immune response. In addition, the effector portion of the Ab can interact with various components of CC the human immune system, including complement.

SQ Sequence 137 AA:

```
Query Match           85.2%; Score 580.5; DB 18; Length 137;  
Best Local Similarity   85.0% ; Pred. No. 3.3e-39;  
Matches 113; Conservative    8; Mismatches 11; Indels 1; Gaps
```

I.

```
OY      1 KDSQAQVLILLAWSGTCGDIVLTQS PDSLAVSLGERATISCKSSQSILNSRTRENYLA 60  
       ||::|||::| | ::||||::::| ::|||::| ::|||::| ::|||:  
Ddb     5 mesqfgyvllmslflfwsgtcgdltvmgspdsalvsjgeratlncksqsllhsngnknytl 64  
  
OY      61 WTQQKPGGPPKKLLTWASTRESGVDPDRSAGSCGTDFTLITISSLOAEDVAAYVCCTQSYNL 120  
       |||::|::| ::|||::| ::|||::| ::|||::| ::|||::|  
Db      65 wygkpgygpkklllywastresgvdpdrfsagsgtcdfitlislaqedavayycqndysy 124  
  
OY      121 -YTFGGTGVEIK 132  
       |||::|::| ::|||::| ::|||::| ::|||::| ::|||::|  
Db      125 pltfggglkvleik 137
```

RESULT 6
WI0544 WI0544 standard; Protein: 137 AA.

AC WI0544;

DT 25-SEP-1997 (first entry)

DE Humanised murine anti-E-selectin antibody CY1788V(LA).

[illegible]

XX	Humanised antibody HuCC49 light chain variable region.
DE	
XX	Humanised antibody; monoclonal antibody; CC49; HuCC49; CDR;
KM	complementarily determining region; mouse; human; carcinoma;
KM	colon cancer; tumor associated glycoprotein-72; TAG-72;
KM	tumour marker; diagnosis; therapy.
XX	
OS	Chimeric - Mus musculus.
OS	Chimeric - Homo sapiens.
XX	
FH	Key
FT	Region
FT	Location/Qualifiers
FT	44..59
FT	/note= "CDR1"
FT	Region
FT	76..82
FT	/note= "CDR2"
FT	Region
FT	115..123
FT	/note= "CDR3"
XX	
PN	WO200026394-A1.
XX	
PD	11-MAY-2000.
XX	
PF	29-OCT-1999; 99WO-US25552.
XX	
PR	31-OCT-1998; 98US-0106534.
PR	02-NOV-1998; 98US-0106757.
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX	
PI	Kashmiri SVS, Padlan EA, Schlom J;
XX	
DR	WPI; 2000-365637/31.
XX	
PT	Chimeric variants of CC49 monoclonal antibodies useful for detecting
PT	and treating cancers associated with the expression of the pancreatic
PT	tumor-associated antigen TAG-72 -
XX	
PS	Disclosure: Fig 4; 76pp; English.
XX	
CC	The present sequence is that of the light chain variable region
CC	(VL) of huCC49, a humanised monoclonal antibody (Mab) formed by
CC	grafting hypervariable regions from murine Mab CC49 into VL and VH
CC	frameworks of human MAb5 LEN and 21/28' CL, respectively, while
CC	retaining murine framework residues required for integrity of the
CC	antigen combining site structure. HuCC49 binds to the human
CC	pancarcinoma tumor associated glycoprotein-72 (TAG-72), which is
CC	found on the surface of certain human tumours. The invention is
CC	directed towards mouse-human chimeric variants of CC49 Mabs with
CC	minimal murine content, to methods of making such variants, and
CC	their therapeutic application. The invention provides
CC	complementarily determining region (CDR) variants of huCC49 in
CC	which fewer than all 6 CDRs of CC49 are present, and specificity
CC	determining region (SDR) variants of huCC49 in which only SDRs of
CC	at least 1 CDR from CC49 are present. Particular variants of HuCC9
CC	have either L-CDR1 and/or L-CDR2 from human Mab LEN. These
CC	variants have the same or 2-fold lower affinity constant than
CC	HuCC49. Other variants additionally have corresponding human
CC	residues at position 97 of L-CDR3, and positions 60, 61, 62 and 64
CC	of H-CDR2. The variants are used in claimed methods of treating
CC	cancer and for detecting cancer cells that express TAG-72.
XX	
SO	Sequence 137 AA:

Query Match 83.3%; Score 567.5; DB 21; Length 137;

Best Local Similarity 82.7%; Pred. No. 3,5e-38;

Matches 110; Conservative 11; Mismatches 11; Indels 1; Gaps 1.

1 MDSQAVLILLILMTWVSGTGGDYLIVLQSPSLAVSLGGERATICKSSQSILNRTRENYIA 60

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

1 mdsqgavlmllllvsgtgdvlvmspspslavslgervtlcnckssqsllysgnqknyia 60

QY	61	WTQOKPGQEPKLLIYWASTRESGVDPFRSGSGGTDFTLTISLSLOAEDVAVYCTQSYNL	120
DB	61	WYQGPp9sgspklllywasaresgvpdrftsgsggtdftltissvqadavayycqgyysy	120
QY	121	-YTFGQGTKEIK	132
DB	121	pltfagckleik	133
RESULT	8		
ID	R59509	standard; Protein; 133 AA.	
AC	R59509;		
DT	31-DEC-1994	(first entry)	
DE	Sequence of the light chain variable region of the mouse NA-8		
DE	antibody, including the signal sequence and mature chain.		
XX			
KW	Antibody NA-8; human CD18; complementarity determining region; CDR;		
OS	Mus musculus.		
FH	Key	Location/Qualifiers	
FT	Protein	21..133	
FT		/label= Mature light chain	
XX	WO9412214-A.		
PN	09-JUN-1994.		
PD			
XX			
XX	30-NOV-1993;	93WO-US11611.	
PE			
XX			
PR	01-DEC-1992;	92US-0983949.	
XX			
PA	(PROT-) PROTEIN DESIGN LABS INC.		
XX			
PI	Co MS, Landolfi NF;		
XX			
DR	WPI; 1994-199973/24.		
DR	N-PSDB; Q66845.		
XX			
PT	New humanised antibodies specific for CD18 - derived from new		
PT	murine antibody NA-8, prevent binding of neutrophils to		
PT	endothelial cells, useful for treating inflammation		
XX			
PS	Disclosure; Flg 1A; 50pp; English.		
XX			
CC	The mouse antibody NA-8 binds to human CD18. cDNAs for the heavy		
CC	chain and light chain variable domain genes of NA-8 were cloned		
CC	and anchored PCR. The cDNA variable domain sequences and the		
CC	deduced AA sequences are shown in Q66845/R59509 and Q66846/R59510.		
XX			
XX	Sequence	133 AA;	
QY	Query Match	82.2%; Score 559.5; DB 15; Length 133;	
	Best Local Similarity	80.5%; Pred. No. 1.5e-37;	
	Matches 107; Conservative 15; Mismatches 10; Indels 1; Gaps	1;	
DB	1	MDSQAOVILILLAWSGTGDIVLTQSPDSLAVSGERRATICKSSQSLNSRTRENYLA	60
	1	msdsgavmllllwvsgtclvmqspsslavsvgekvmsckssqsllysqknyla	60
QY	61	WTQOKPGQEPKLLIYWASTRESGVDPFRSGSGGTDFTLTISLSLOAEDVAVYCTQSYNL	120
DB	61	WYQGPp9sgspklllywasaresgvpdrftsgsggtdftltissvqadavayycqgyysy	120
QY	121	-YTFGQGTKEIK	132
DB	121	pltfagckleik	133

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RESULT      9
P80894
ID          P80894 standard; protein; 133 AA.
AC          P80894;
DT          03-DEC-1990 (first entry)
XX          V region of L chain of anti-P.aeruginosa exotoxin Ab #1.
DE          Pseudomonas aeruginosa; anti-exotoxin antibody; L chain; V region;
KM          ds.
XX          Homo sapiens.
OS          Homo sapiens.
XX          Key
FH          Peptide
FT          1..20
FT          /label=signal peptide
FT          21..133
FT          /label=V region of L chain
XX          EP270077-A.
XX          PD
XX          08-JUN-1988.
XX          PE
XX          01-DEC-1987; 87EP-0117760.
XX          PR
XX          03-DEC-1986; 86JP-0288340.
XX          PR
XX          26-NOV-1987; 87JP-0298513.
XX          PA
XX          (SUMO ) SUMITOMO CHEM IND KK.
XX          PI
XX          Nakatani T, Momura N, Horigome K, Noguchi H;
DR          WPI: 1988-156310/23.
DR          N-PSDB: N80499.
XX          PT
XX          New gene encoding for antibody to Pseudomonas aeruginosa exotoxin -
PT          plus recombinant vectors and host cells, useful for treating
PT          infections.
XX          PS
XX          Claim 4: Page 25; 39pp; English.
XX          CC
XX          Sequence is variable region of light chain of anti-exotoxin
XX          antibody with signal sequence. N80498 encodes the same sequence
XX          except that its signal peptide encoding sequence contains an
XX          intron.
XX          CC
XX          See also N80495-N80496, N80498 and N80941-2.
XX          SQ
XX          Sequence 133 AA;

Query Match      81.9%; Score 557.5; DB 9; Length 133;
Best Local Similarity 84.6%; Pred. No. 2,1e-37;
Matches 110; Conservative 6; Mismatches 13; Indels 1; Gaps 1.

OY      4 QAOVILLILWWSGCGDVLTFQSPDSLAVSLGERATISCKSSQSILNRTRENTLAWYQ 63
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      4 qgvvtislltwsgygdltvmcgsposslavslgeratlnckssqsvlysnknylawYq 63
OY      64 QKPGPPKLLIYWASTRESGVDPDRSGSGGDTFTLTISSLQAEDEVAVVYCTQSYNL-VT 122
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      64 qkpqpgpklllywastresgydpdrtsrgsgsgtdftltisslqaedvavyycqgyslpt 123
OY      123 FGQGTKEVEIK 132
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      124 fgggtkveik 133
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT      10
W06206
ID          W06206 standard; protein; 134 AA.

```

XX	W06206;		
AC	17-FEB-1997	(first entry)	
XX	Xenograft antibody HAR-1	kappa light chain variable region.	
XX	Xenograft rejection; xenotransplantation; organ transplant;		
XX	animal model; hamster; monoclonal antibody; HAR-1.		
KW			
XX	Rattus sp.		
OS			
XX	Key	Location/Qualifiers	
FT	Region	1..20	
FT		/label= Leader	
FT	Region	21..43	
FT		/label= FR-1	
FT		/note= "framework region 1"	
FT	Region	44..60	
FT		/label= CDR-1	
FT		/note= "complementarity determining region 1"	
FT	Region	61..75	
FT		/label= FR-2	
FT		/note= "framework region 2"	
FT	Region	76..82	
FT		/label= CDR-2	
FT		/note= "complementarity determining region 2"	
FT	Region	83..114	
FT		/label= FR-3	
FT		/note= "framework region 3"	
FT	Region	115..122	
FT		/label= CDR-3	
FT		/note= "complementarity determining region 3"	
FT	Region	123..134	
FT		/label= FR-4	
FT		/note= "framework region 4"	
PN	W09636358-A1.		
PD	21-NOV-1996.		
XX	14-MAY-1996;	96W0-US06804.	
PE	15-MAY-1995;	95US-0440621.	
XX	(CEDA-) CEDARS SINAI MEDICAL CENT.		
PA	Cramer DV, Makowka L, Wu G;		
XX	WPI: 1997-011852/01;		
DR	N-PSDB; T43415.		
XX	Inhibiting xenograft rejection by modifying antigen expression of		
PT	the graft - prevents binding of anti-donor antibody and prolongs		
PT	graft survival		
PS	Claim 11; Page 99; 135pp; English.		
XX	A polypeptide (W06206) comprises the kappa light chain variable		
CC	region of the LEW rat anti-hamster xenograft monoclonal antibody		
CC	HAR-1. It is encoded by a cDNA clone (T43415) obtd. from a HAR-1		
CC	hybridoma light chain cDNA library; the hybridoma was produced by		
CC	fusing spleen cells of a LEW rat that had received a hamster heart		
CC	transplant, with rat myeloma cells. Recombinant fragments, e.g.		
CC	F(ab') ₂ and Fab', of the antibody block binding of preformed		
CC	anti-donor xenograft antibodies in a recipient animal serum to		
CC	antigen expressed by endothelial cells of the xenograft, i.e. they		
CC	inhibit antibody-mediated rejection, thereby prolonging the		
CC	survival of the hamster xenograft in the recipient.		
XX	Sequence 134 AA;		

Query Match	81.8%;	Score 557;	DB 18;	Length 134;
Best Local Similarity	78.8%;	Pred. No. 2.3e-37;		
Matches 104;	Conservative 14;	Mismatches 14;	Indels 0;	Gaps 0;
OY	1	MDSOAVLILLLWVSGTGDIVLQSPDSLAVSLGERATISCKSSQSILNRTRENTYLA 60		
DB	1	mesqgvlmslllwsqgclvmtqtpssqvasqekvmsckssqsllynenknyla 60		
OY	61	WTQKPGCPKLLIYWASTRESGVDPDRFGSGSGGTFILITLSSLOAEDVAVYCTQSTNL 120		
DB	61	wyrqpgpsgpklllywastresgvpdrfrysgsgtdflltllssvgaedlaavycqgyyl 120		
OY	121	YTFGGTKEIK 132		
DB	121	ylfagqtklelk 132		
RESULT	11			
ID	Y24374	standard; Protein; 141 AA.		
XX	XX			
AC	Y24374;			
XX	XX			
DT	17-SEP-1999	(first entry)		
XX	XX			
DE	Human monoclonal antibody against CTGF SEQ ID NO:16.			
XX	XX			
KW	Human monoclonal antibody; connective tissue growth factor; CTGF;			
KM	cell proliferation disorder; fibrosis; liver cirrhosis; nephritis;			
KW	skin ulcer; keloid; rheumatoid arthritis; hepatitis; cancer;			
KM	rheumatic vascular inflammation.			
XX	XX			
OS	Homo sapiens.			
XX	XX			
PN	W0933878-A1.			
PD	08-JUL-1999.			
XX	XX			
PF	16-DEC-1998;	98WO-JP05697.		
XX	XX			
PR	15-DEC-1998;	98JP-0356183.		
PR	25-DEC-1997;	97JP-0367699.		
XX	XX			
PA	(NIBS) JAPAN TOBACCO INC.			
XX	XX			
PI	Sakamoto S., Takigawa M., Tamatani T., Tezuka K;			
XX	XX			
DR	WPI: 1999-430232/36.			
DR	N-PSDB: X90025.			
XX	XX			
PT	New monoclonal antibody reactive with connective tissue growth			
PT	factor useful in the treatment of cell proliferation disorders			
XX	XX			
PS	Claim 18; Page 191-192; 212pp; Japanese.			
XX	XX			
CC	X90020 to X90029 encode monoclonal antibodies which react with human			
CC	connective tissue growth factor (CTGF). Y24369 to Y24378 represent			
CC	these monoclonal antibodies. The antibodies are useful in the diagnosis,			
CC	prevention and treatment of cell proliferation disorders in which CTGF			
CC	is implicated, including fibrosis of lung, kidney, liver and other			
CC	tissues; liver cirrhosis; nephritis; skin ulcers and keloid; rheumatoid			
CC	arthritis; rheumatic vascular inflammation; hepatitis; and cancer.			
XX	XX			
SQ	Sequence 141 AA;			
Query Match	81.5%;	Score 555;	DB 20;	Length 141;
Best Local Similarity	82.4%;	Pred. No. 3.5e-37;		
Matches 108;	Conservative 9;	Mismatches 12;	Indels 2;	Gaps 14;
OY	4	GAQVILLLWVSGCGDVLVLTQSPDSLAVSLGERATISCKSSQSILNRTRENTYLA 63		
DB	4	qgqvflsilwvsgvgdvlvmtqspdslavslgeratlnckssqvllysnmknylawyq 63		

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OY 64 OKPPGPKLLIYMASTRSGVDPFRSGSGSGDFFLLTSSLOAEVAVAYYCQSNL--Y 121
Db 64 qkpggpklllywastrsgvdpfrtsgsgsgdftlltsslgadavayycqgqytlppw 123
OY 122 TFGGCTKWEIK 132
Db 124 tfggctkweik 134

RESULT 12
B03714
B03714 standard; protein; 135 AA.
B03714;
04-OCT-2000 (first entry)
Immunoglobulin kappa2 amino acid sequence fragment.
KW Aortic aneurysm-associated antigen protein; AAP; microfibrillar protein;
KW abdominal aortic aneurysm disease; treatment; detect; tolerance;
KW Immunoglobulin kappa; 19k.
XX Unidentified.
XX OS
XX PN
XX US6048704-A.
XX PD
XX 11-APR-2000.
XX PF
XX 07-MAR-1997; 97US-0812586.
XX PR
XX 07-MAR-1996; 96US-0012976.
XX PA
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX PI
XX Tilson MD:
XX WPI: 2000-316895/27.
XX DR
XX Isolated microfibrillar protein for alleviating abdominal aortic
XX PT aneurysm disease is purified from human aortic tissue and binds
XX PR immunoreactively with immunoglobulin
XX PS
XX Example 3; Column 30; 70pp; English.
XX PS
XX The present invention relates to an isolated microfibrillar protein of
XX CC approximately 40KD. The protein is isolated from human aortic tissue and
XX CC binds immunoreactively with immunoglobulin purified from human abdominal
XX CC aortic aneurysm (AAA) tissue. The protein is referred to as aortic
XX CC aneurysm-associated antigenic protein (AAP). The protein is capable of
XX CC forming a disulphide bonded dimer. The protein is immunoreactive with
XX CC human kappa immunoglobulin. Also included in the invention are
XX CC recombinantly produced human AAA proteins. AAP shows regions of homology
XX CC with the bovine microfibril associated glycoprotein MFAP-4 and also with
XX CC fibronogen and vitronectin. The isolated microfibrillar protein is useful
XX CC for alleviating abdominal aortic aneurysm (AAA) disease and detecting the
XX CC presence of AAA-associated immunoglobulin bound to the human aortic
XX CC tissue. Antibodies directed against AAP can be used to detect AAA
XX CC disease. The recombinant protein can be used to induce tolerance to
XX CC antigenic AAA protein in the subject e.g. human. This sequence represents
XX CC an immunoglobulin kappa2 amino acid sequence. The sequence shares
XX CC homology with the AAP of the invention, it was used to identify and
XX CC characterise AAP.
XX CC
XX Sequence 135 AA:

Query Match 81.3%; Score 553.5; DB 21; Length 135;
Best Local Similarity 84.6%; Pred. No. 4,5e-37;
Matches 110; Conservative 5; Mismatches 14; Indels 1; Gaps 1;

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PD 03-NOV-1999.
 XX
 PF 30-APR-1998; 98EP-0107925.
 XX
 PR 30-APR-1998; 98EP-0107925.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 XX
 PI Park JF, Garin-Chesa P, Bamberger U, Leger O, Saldanha J;
 PI Rectig MJ;
 XX
 DR WPI: 1999-621833/54.
 DR N-PSDB: 232784.
 XX
 PT New antibody protein, useful for treating cancer and for imaging
 PT presence of activated stromal fibroblasts in healing wound or inflamed
 PT skin -
 XX
 PS Example 3; Fig 30; 143pp: English.
 XX
 CC This sequence represents the light chain (version a) of a reshaped human
 CC F19 antibody. F19 (ATCC Accession number HB 8269) is a murine monoclonal
 CC antibody against fibroblast activation protein alpha (FAP). FAP is a cell
 CC surface molecule of reactive stromal fibroblasts, and its induction
 CC is a highly consistent molecular trait of the reactive stroma of many
 CC types of epithelial cancer. Although F19 may be useful in vitro, e.g.,
 CC for diagnosis, its applications for in vivo use in humans are problematic
 CC as it elicits a human anti-mouse response which reduces the efficacy of
 CC the antibody in patients and impairs continued administration. The
 CC novel human reshaped F19 was humanised by grafting the murine
 CC complementarity determining regions (CDRs) of F19 onto human variable
 CC region framework sequences, and then joining these "reshaped human"
 CC variable regions to human constant regions. These modifications
 CC also result in the improved producibility in eukaryotic cell culture
 CC systems as compared to a chimeric antibody having the entire variable
 CC regions of F19 joined to human constant regions. The human reshaped F19
 CC antibody has low immunogenicity for humans and is useful for treating
 CC cancers e.g., colorectal cancers, non-small cell lung cancers, breast
 CC cancers, head and neck cancers, ovarian cancers, lung cancers, bladder
 CC cancers, pancreatic cancers and metastatic cancers. It is also useful for
 CC the detection of activated stromal fibroblasts in a healing wound,
 CC inflamed skin or a tumour in a human patient.
 CC
 SQ Sequence 240 AA:
 XX
 Query Match 80.4%; Score 547.5; DB 20; Length 240;
 Best Local Similarity 82.1%; Pred. No. 2.3e-36;
 Matches 110; Conservative 10; Mismatches 11; Indels 3; Gaps 2;
 QY 1 MDSQAQVLLILLMWSTGCDIVLTQSPDSLAVSLGERATISCKSSQSLNSRTRENYLA 60
 Db 1 mecdlllwlwllwvpgsgdlyvmtspdsldvslgeratlnssqsllysrnqkyla 60
 QY 61 WYQQRPGQPKLLIYMASTRESGVPDRFSSGSGTDTLTITSSLOADVAIVYCTQ--SY 118
 Db 61 wygqkpgqpklllywastresgyvdrfssgsgtdltltltslsgaedvavvyccqgyfsy 120
 QY 119 NLTFGQGTKEIK 132
 Db 121 pl-tfgqgtkveik 133
 RESULT 15
 R85909
 ID R85909 standard; Protein; 133 AA.
 XX
 AC R85909;
 XX
 DT 02-JUL-1996 (first entry)
 XX
 DE Monoclonal antibody, CB-Hep.1, light chain variable domain.

KW HBV; hepatitis B virus surface antigen; monoclonal; antibody;
 KW CB-Hep.1; immunopurification; detection; hybridoma; recombinant;
 KW Fv; variable; VH; HBsAg.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /label= sig_peptide
 FT Protein 21..133
 FT /label= mat_protein
 FT Domain 21..43
 FT /label= FR1
 FT Domain 44..60
 FT /label= CDR1
 FT Domain 61..75
 FT /label= FR2
 FT Domain 76..82
 FT /label= CDR2
 FT Domain 83..114
 FT /label= FR3
 FT Domain 115..123
 FT /label= CDR3
 FT Domain 124..133
 FT /label= FR4
 XX
 PN EP686696-A1.
 XX
 PD 13-DEC-1995.
 XX
 PF 09-JUN-1995; 95EP-0201535.
 PF 09-JUN-1994; 94CU-0000073.
 PR (ING-) CENT ING GENETICA & BIOTECNOLOGIA.
 PA (KAMB/) KAMBEEL R W.
 PA Ayala Avila MA, Canaan-Haden Frias LM, del Carmen Dominguez Horta MC;
 PI Fernandez de Cossio Dorta-Dugue ME, Gavilondo Cowley JVC;
 XX
 DR WPI: 1996-021914/03.
 DR N-PSDB: Q74067.
 XX
 PT New recombinant single chain Fv antibody fragment - useful for
 PT immuno-purificn. and detection of HBsAg
 XX
 PS Claim 1; Page 19; 23pp: English.
 XX
 CC R85908 and R85909 are the heavy and light chain variable domains of
 CC the murine hybridoma-derived monoclonal antibody CB-Hep.1 Fv region.
 CC The heavy and light chain regions are used to produce a recombinant
 CC antibody fragment having specificity for the hepatitis B virus
 CC surface antigen (HBsAg). The recombinant antibody may be used for
 CC immunopurification of HBsAg, in immunoassays for the detection of
 CC HBsAg and for insolubilisation of heterologous fusion proteins
 CC expressed in E. coli aiding their purification.
 CC
 SQ Sequence 133 AA:
 XX
 Query Match 80.0%; Score 544.5; DB 17; Length 133;
 Best Local Similarity 78.2%; Pred. No. 2.3e-36;
 Matches 104; Conservative 14; Mismatches 14; Indels 1; Gaps 1;
 QY 1 MDSQAQVLLILLMWSTGCDIVLTQSPDSLAVSLGERATISCKSSQSLNSRTRENYLA 60
 Db 1 mdsqayvlmlwllwvsgcdlyvmsgpslavsgekvslckssqsllylnhbkyla 60
 QY 61 WYQQRPGQPKLLIYMASTRESGVPDRFSSGSGTDTLTITSSLOADVAIVYCTQSYNL 120
 Db 61 wfqgkpgqpklllywastresgyvdrfssgsgtdltltltsvkaedlavvyccqgyyny 120
 QY 121 -YTFGQGTKEIK 132

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Db 121 pytf99g9tklelk 133

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